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? s triton

      S4   28189  TRITON
? ds


Set     Items   Description
S1        988   DETERGENT AND (NON-IONIC OR ANIONIC)
S2         31   S1 AND SARKOSYL
S3         19   RD (unique items)
S4      28189   TRITON
? s s4 and s1

           28189  S4
             988  S1
      S5     163  S4 AND S1
? rd

...examined 50 records  (50)
...examined 50 records  (100)
...examined 50 records  (150)
...completed examining records
      S6     117  RD (unique items)
? s s3 and s6

              19  S3
             117  S6
      S7       4  S3 AND S6
? t s7/3,ab/all


 7/3,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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08416349   95164518
  Architecture of the cell envelope of Chlamydia psittaci 6BC.
  Everett KD; Hatch TP
  Department of Microbiology and Immunology, University of Tennessee,
Memphis 38163.
  J Bacteriol (UNITED STATES)  Feb 1995,  177 (4) p877-82,  ISSN 0021-9193
Journal Code: HH3
  Contract/Grant No.: AI19570, AI, NIAID
  Languages: ENGLISH
  Document type: JOURNAL ARTICLE
  The cysteine-rich envelope proteins of the elementary body form of
chlamydiae are thought to be located in the outer membrane on the basis of
their insolubility in the weak anionic detergent N-lauryl
sarcosinate (Sarkosyl ). We found, however, that the insolubility of
the small (EnvA) and the large (EnvB) cysteine-rich proteins of Chlamydia
psittaci 6BC in Sarkosyl is dependent on the maintenance of a
supramolecular disulfide-cross-linked complex and is unlikely to be a valid
indicator of outer membrane location. Consequently, we used other methods
to characterize the architecture of the cell envelope of C. psittaci 6BC.
We found that disulfide-reduced EnvA, previously shown to be a lipoprotein,
segregated into the detergent phase during Triton X-114
partitioning experiments and was recovered from the membrane fraction of
elementary bodies lysed by nondetergent means. In contrast,
disulfide-reduced EnvB segregated to the aqueous phase in partitioning
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lysed in the absence of detergents. The hydrophobic affinity probe 3-(trifluoromethyl)-3-(m-[125I]iodophenyl)-diazirine labeled the major outer membrane protein and EnvA but did not label EnvB. Treatment of intact elementary bodies of C. psittaci with trypsin had no effect on the cysteine-rich proteins, although the major outer membrane protein was partially degraded. On the basis of these and other observations, we propose that EnvA is anchored to the outer membrane by its lipid moiety, with a hydrophilic peptide portion extending into the periplasm, and that EnvB is located exclusively within the periplasm. We further propose that disulfide-cross-linked polymers of EnvB are the functional equivalent of peptidoglycan, forming a disulfide-cross-linked network with the periplasmic domains of EnvA and other membrane proteins, which accounts for the osmotic stability of elementary bodies.

7/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06406090 90277695
Solubilization of the 97-kDa native form of liver microsomal 3-hydroxy-3-methylglutaryl-coenzyme A reductase.
Vermilion JL; Schroepfer GJ Jr
Department of Biochemistry and Cell Biology, Rice University, Houston, Texas 77251-1892.
J Biol Chem (UNITED STATES) Jun 15 1990, 265 (17) p9984-92, ISSN 0021-9258 Journal Code: HIV
Contract/Grant No.: HL-15376, HL, NHLBI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Liver microsomal 3-hydroxy-3-methylglutaryl-CoA reductase was partially purified from cholestyramine-fed rats by sequential extraction of the membrane with 3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulfonate (CHAPS) and polyethylene glycol nonylphenyl ether (**Triton** N-101) and solubilized by incorporation of the resulting insoluble protein preparation into a **detergent** mixture of **Triton** N-101 and sodium N-lauroylsarcosinate (**Sarkosyl**) in the presence of high salt. The purification procedure resulted in approximately a 3-4-fold increase in specific activity compared with the microsomal fraction, and the enzyme was recovered with yields as high as 63%. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis and a blotting experiment using antiserum to the purified 53,000-dalton reductase fragment showed that the major immunoreactive polypeptide had a Mr of 97,000, that expected for the native intact form of the enzyme (Chin, D. J., Gil, G., Russell, D. W., Liscum, L., Luskey, K. L., Basu, S. K., Okayama, H., Berg, P., Goldstein, J. L., and Brown, M. S. (1984) Nature 308, 613-617). In addition, the effect of various detergents on the activity and stability of the membrane-bound and the partially purified enzyme was determined, and a method for protection of the reductase from inactivation caused by the addition of **anionic** detergents to the assay mixture is described.

7/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03413604 81191028
Purification and partial characterization of the major outer membrane protein of Chlamydia trachomatis.
Caldwell HD; Kromhout J; Schachter J
Infect Immun (UNITED STATES) Mar 1981, 31 (3) p1161-76, ISSN 0019-9567 Journal Code: GO7
Contract/Grant No.: EY 03046, EY, NEI; EY 01198, EY, NEI; EY 02216, EY, NEI; +

Document type: JOURNAL ARTICLE

Elementary bodies (EB) of Chlamydia trachomatis serotypes C, E, and L2 were extrinsically radioiodinated, and whole-cell lysates of these serotypes were compared by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE). Autoradiography of the polypeptide profiles identified a major surface protein with an apparent subunit molecular weight of 39,500 that was common to each C. trachomatis serotype. The abilities of nonionic (**Triton** X-100), dipolar ionic (Zwittergent TM-314), mild (sodium deoxycholate and sodium N-lauroyl sarcosine), and strongly **anionic** (SDS) detergents to extract this protein from intact EB of the L2 serotype were investigated by SDS-PAGE analysis of the soluble and insoluble fractions obtained after each **detergent** treatment. Only SDS readily extracted this protein from intact EB. **Sarkosyl** treatment selectively solubilized the majority of other EB proteins, leaving the 39,500-dalton protein associated with the **Sarkosyl** -insoluble fraction. Ultrastructural studies of the **Sarkosyl**-insoluble EB pellet showed it to consist of empty EB particles possessing an apparently intact outer membrane. No structural evidence for a peptidoglycan-like cell wall was found. Morphologically these chlamydial outer membrane complexes (COMC) resembled intact chlamydial EB outer membranes. The 39,500-dalton outer membrane protein was quantitatively extracted from COMC by treating them with 2% SDS at 60 degrees C. This protein accounted for 61% of the total COMC-associated protein, and its extraction resulted in a concomitant loss of the COMC membrane structure and morphology. The soluble extract obtained from SDS-treated COMC was adsorbed to a hydroxylapatite column and eluted with a linear sodium phosphate gradient. The 39,500-dalton protein was eluted from the column as a single peak at a phosphate concentration of approximately 0.3 M. The eluted protein was nearly homogeneous by SDS-PAGE and appeared free of contaminating carbohydrate, glycolipid, and nucleic acid. Hyperimmune mouse antiserum prepared against the 39,500-dalton protein from serotype L2 reacted with C. trachomatis serotypes Ba, E, D, K, L1, L2, and L3 by indirect immunofluorescence with EB but failed to react with serotypes A, B, C, F, G, H, I, and J, with the C. trachomatis mouse pneumonitis strain, or with the C. psittaci feline pneumonitis, guinea pig inclusion conjunctivitis, or 6BC strains. Thus, the 39,500-dalton major outer membrane protein is a serogroup antigen of C. trachomatis organisms.

7/3,AB/4 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

03671923 BIOSIS NO.: 000074087500
EFFECTS OF DETERGENTS AND DIVALENT CATIONS ON THE FUNCTIONING OF CELL ENVELOPES OF ESCHERICHIA-COLI IN THE EARLY STAGES OF INFECTION WITH BACTERIO PHAGE PHI-X-174
AUTHOR: MANO Y; KAWABE T; OBATA K; YOSHIMURA T; KOMANO T
AUTHOR ADDRESS: LABORATORY BIOCHEMISTRY, DEP. AGRICULTURAL CHEMISTRY, KYOTO UNIV., KYOTO 606, JPN.
JOURNAL: AGRIC BIOL CHEM 46 (3). 1982. 631-638.
FULL JOURNAL NAME: Agricultural and Biological Chemistry
CODEN: ABCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Effects of detergents and divalent cations (Ca2+, Mg2+) on intact cells and envelope fraction I of E. coli were examined by measuring the eclipse kinetics of bacteriophage .vphi.X174 and by polyacrylamide gel electrophoresis of cell envelope proteins. Cell envelopes having receptor activity to convert .vphi.X174 to eclipsed particles (eclipsing activity) were destroyed by cationic **detergent** cetyl trimethyl ammonium bromide (CTAB) and **anionic detergent** N-lauroyl sarcosine sodium salt (**Sarkosyl**), but were not destroyed by many nonionic detergents, such as **Triton** X-100, Pluronic P103, Brij 58, Tween 20

detergent Span 80 caused [redacted]e disruption of cell envelopes [redacted] the presence of a low concentration (1 mM) of divalent cations, but not in the presence of a higher concentration (5 mM) of divalent cations. Divalent cations were shown to stabilize the cell envelope structure and

s s6 and rna

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           117  S6
        587936  RNA
     S8       5  S6 AND RNA
? t s8/3,ab/all
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8/3,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09674742 96256733
Enzymatic characterization of hepatitis C virus NS3/4A complexes expressed in mammalian cells by using the herpes simplex virus amplicon system.
Hong Z; Ferrari E; Wright-Minogue J; Chase R; Risano C; Seelig G; Lee CG; Kwong AD
Antiviral Chemotherapy and Structural Chemistry Departments, Schering-Plough Research Institute, Kenilworth, New Jersey 07033-0539, USA.zhi.hong@spcorp.com
J Virol (UNITED STATES) Jul 1996, 70 (7) p4261-8, ISSN 0022-538X
Journal Code: KCV
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The hepatitis C virus (HCV) NS3 protein possesses three enzymatic activities: an N-terminal serine protease activity, a C-terminal **RNA** -stimulated NTPase activity, and an **RNA** helicase activity. To characterize them, the full-length NS3(631)/4A and three C-terminal truncated proteases (NS3(201)/4A, NS3(181)/4A, and NS3(155)/4A were expressed in mammalian cells with HSV amplicon-defective viruses. Our results revealed that all of the NS3/4A proteins produced in mammalian cells (except NS3(155)/4A) are active in processing both cis and trans cleavage sites. Temperature optimization studies revealed that the protease is more active at temperatures ranging from 4 to 25 degrees C and is completely inactive at 42 degrees C. The **RNA**-stimulated ATPase activity was characterized with a partially purified NS3(631)/4A fraction and has a higher optimal temperature at 37 to 42 degrees C. The effects of detergents on both NS3 protease and **RNA** -stimulated ATPase were similar. Nonionic detergents such as **Triton** X-100, Nonidet P-40 and Tween 20 did not affect the activities, while **anionic** detergents such as sodium dodecyl sulfate and deoxycholic acid were inhibitory. Zwitterionic **detergent** such as 3-[(3-cholamidopropyl)-dimethyl-ammoniol-1-propanesulfonate (CHAPS) inhibited protease activity at a concentration of 0.5% (8 mM), which had no effect on ATPase activity. Finally, **RNA** -unwinding activity was demonstrated in the NS3(631)/4A fraction but not in the similarly purified NS3(181)/4A and NS3(201)/4A fractions. NS(363)/4A unwinds **RNA** duplexes with 3' but not 5' single-stranded overhangs, suggesting that the NS3 **RNA** helicase functions in a 3'-to-5' direction.

8/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05850710 86182143
A disappearance of a 24-kDa acid-soluble protein from liver chromatin of normal and starved hens following D-galactosamine administration.

Palyga J
Z Naturforsch [C] (GERMA[redacted] WEST) Nov-Dec 1985, 40 (1[redacted]2) p798-805, ISSN 0341-0382 Journal Code: XYX
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Normal and starved adult chickens were injected intraperitoneally with D-galactosamine hydrochloride (0.5 g/kg body weight) and 6 h later liver chromatin acid-soluble proteins were isolated. These proteins were resolved by a two-dimensional polyacrylamide gel electrophoresis in the presence of non-ionic **detergent**, **Triton** X-100, in the first dimension and **anionic detergent**, sodium dodecyl sulfate, in the second dimension. Although spotting patterns of acid-soluble chromatin proteins were remarkably similar between normal and starved control birds and those receiving D-galactosamine, a disappearance of a 24-kDa protein after administration of this agent was found. Moreover, it was shown that this protein was also completely absent in the chicken erythrocyte chromatin which was known to be inactive in **RNA** synthesis. It seems that the disappearance of the 24-kDa chromatin protein may be associated with inhibiting of transcription in hen liver after D-galactosamine administration and during hen erythrocyte maturation.

8/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03835719 81095800
Experimental scrapie in the mouse: electrophoretic and sedimentation properties of the partially purified agent.
Prusiner SB; Garfin DE; Cochran SP; McKinley MP; Groth DF; Hadlow WJ; Race RE; Eklund CM
J Neurochem (ENGLAND) Sep 1980, 35 (3) p574-82, ISSN 0022-3042 Journal Code: JAV
Contract/Grant No.: NS-14069, NS, NINDS
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Some biochemical and biophysical properties of the scrapie agent in a partially purified fraction P5 from murine spleen are described in this communication. The agent was stable in the nonionic detergents **Triton** X-100 and Nonidet P40 and stable in the nondenaturing, **anionic** detergents sodium cholate and sodium N-lauroyl sarcosinate. In contrast, sodium dodecyl sulfate (SDS) inactivated the agent at high concentrations (1% or >) when the **detergent**-to-protein ration approached 1.5 g SDS/g protein. The agent was resistant to inactivation by nucleases and proteases, even in the presence of 0.1% SDS. A broad peak of infectivity was exhibited in modified colloidal silica (Percoll) density gradients. Maximal titers were found at a Percoll density of 1.10 g/cm3 in the presence and absence of 0.05% SDS. Gel electrophoresis of the agent in the presence of 0.1% SDS resulted in inactivation of > 95% of the agent loaded onto the gel. Free-flow electrophoresis showed that > 99% of the agent in fraction P5 migrated toward the anode, but not as a discrete species. Sedimentation analysis of the agent in fraction P5 in the presence of 1% lysolecithin showed that the agent has a sedimentation coefficient of < 300S but > 30S. Heating P5 preparations caused the agent to associate with cellular elements and form aggregates with sedimentation coefficients > 10,000S. Removal by differential centrifugation of the large forms of the agent produced upon heating permitted characterization of a discrete subpopulation of scrapie agent particles. Rate-zonal sucrose gradient studies showed that > 95% of the infectivity in this subpopulation sedimented as uniform particles with a sedimentation coefficient of 240S.

8/3,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03016514 76111870
Initiation factors in protein synthesis by free and membrane-bound polyribosomes of liver and hepatoma.
Murty CN; Verney E; Sidransky H
Biochem J (ENGLAND) Oct 1975, 152 (1) p143-51, ISSN 0006-2936
Journal Code: 9YO
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The activity of initiation factors obtained from free and membrane-bound polyribosomes of liver and of transplantable H5123 hepatoma of rats was investigated by using an assay of protein synthesis in vitro in which poly (U)-directed polyphenylalanine synthesis was measured. Initiation factors of membrane-bound polyribosomes prepared by using the **anionic detergent** deoxycholate exhibited less activity in incorporating [14C]phenylalanyltRNA into polypetides than did initiation factors of free polyribosomes. However, when membrane-bound polyribosomes were prepared after using the non-ionic **detergent Triton** X-100, no significant differences in activities in polyphenylalanine synthesis were observed between the initiation factors of free and membrane-bound polyribosomes. These results suggest that **Triton** X-100 is preferable to deoxycholate in the isolation of of initiation factors from polyribosomes. Initiation factors, prepared by using **Triton** X-100, of free polyribosomes of hepatoma exhibited greater activity in the stimulation of polyphenylalanine synthesis than did the initiation factors of free or membrane-bound polyribosomes of host livers or of membrane-bound polyribosomes of hepatomas.

8/3,AB/5 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

01921559 BIOSIS NO.: 000062011653
MOLECULAR ORGANIZATION AND STABILIZING FORCES OF SIMPLE **RNA** VIRUSES
PART 4 SELECTIVE INTERFERENCE WITH PROTEIN **RNA** INTERACTIONS BY USE OF SODIUM DODECYL SULFATE
AUTHOR: BOATMAN S; KAPER J M
JOURNAL: VIROLOGY 70 (1). 1976 1-16.
FULL JOURNAL NAME: Virology
CODEN: VIRLA
RECORD TYPE: Abstract

ABSTRACT: The effect of the **anionic detergent** sodium dodecyl sulfate (SDS) on a number of simple isometric **RNA** viruses and empty capsids was tested. Some viruses showed extreme sensitivity, e.g., cucumber mosaic (CMV), brome mosaic (BMV) and alfalfa mosaic virus; some extreme resistance, e.g., turnip yellow mosaic (TYMV) and tomato bushy stunt virus; and some intermediate resistance, e.g., southern bean mosaic virus and bacteriophage f2, to dissociation into components by this **detergent**. In the viruses most sensitive to SDS, virion dissociation is apparently caused by disruption of the electrostatic protein-**RNA** interactions which are responsible for stabilizing the virions. Dodecyl sulfate (DS-) ions may bind by means of the hydrocarbon chain to specific binding sites on the virion so that the sulfate groups are near lysine (or arginine) phosphate interaction points; these interactions are neutralized and the phosphates are repulsed, resulting in virion dissociation. Based on this hypothesis several predictions were made, tested experimentally and found valid. Virions become more resistant to SDS as the contribution of the protein-protein interactions to virus stability increases. This was confirmed by testing the sensitivities of a number of viruses, including those mentioned above, to SDS. Capsids devoid of nucleic acid are less sensitive to SDS than the respective intact virions. The behavior of TYMV, BMV and bacteriophage f2 virions and capsids with SDS confirmed this prediction. Positive and

viruses. Reassembly of [redacted]uses stabilized by protein-**RNA**[redacted] interactions is inhibited by SDS but not by positive detergents. These predictions were confirmed by appropriate experiments with CMV or BMV and SDS, dodecyltrimethylammonium chloride and **Triton**-X-100. Measurements of amounts of **detergent** bound at low SDS concentrations showed that CMV and BMV have much greater affinities than TYMV for DS- ions. SDS is apparently useful as a probe for protein-**RNA** interactions and relative sensitivity to SDS could be used in categorizing viruses according to stabilizing interactions.

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? b 155, 5

       09apr00 14:33:20 User242957 Session D152.2
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     $0.01  TYMNET
     $0.01  Estimated cost this search
     $0.02  Estimated total session cost   0.198 DialUnits

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  File 155:MEDLINE(R)  1966-2000/Jun W1
         (c) format only 2000 Dialog Corporation
*File 155: MEDLINE will be reloaded. Accession numbers will change.
  File   5:Biosis Previews(R)  1969-2000/Apr W2
         (c) 2000 BIOSIS

      Set  Items  Description
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? s detergent and (non-ionic or anionic)

           40997  DETERGENT
              13  NON-IONIC
           17943  ANIONIC
      S1     988  DETERGENT AND (NON-IONIC OR ANIONIC)
? s s1 and sarkosyl

             988  S1
             814  SARKOSYL
      S2      31  S1 AND SARKOSYL
? rd

...completed examining records
      S3      19  RD (unique items)
? t s3/3,ab/all


 3/3,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

09254098   97128786
  A fusion protein library: an improved method for rapid screening and
characterization of DNA binding or interacting proteins.
  Ikeda M; Arai K; Masai H
  Department of Molecular and Developmental Biology, University of Tokyo,
Japan.
  Gene (NETHERLANDS)   Nov 28 1996,  181 (1-2) p167-71,  ISSN 0378-1119
Journal Code: FOP
  Languages: ENGLISH
  Document type: JOURNAL ARTICLE
  A rapid method for screening and characterization of DNA binding or
protein-interacting molecules is described. The method relies on a fusion
protein library in which randomized DNA fragments are inserted into pGEX-3X
and its derivatives to generate collections of GST-fusion proteins. After
inducing the expression of the fusion proteins by addition of IPTG, the
colonies can be screened either with radioactively labeled DNA/RNA fragment
for specific clones encoding DNA/RNA binding proteins or with an antibody
for clones encoding proteins of interest. They can also be screened with a
radioactively labeled protein for cloning of interacting molecules. The
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conducting the lysis of t[redacted]cells and an affinity column i[redacted]he presence of an alkyl **anionic detergent**, N-laurylsarcosine (**sarkosyl**), and can be further characterized.

3/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09063229 97278510
Expression of EcR and USP in Escherichia coli: purification and functional studies.
Elke C; Vogtli M; Rauch P; Spindler-Barth M; Lezzi M
Institut Fur Zellbiologie, ETH-Honggerberg, Zurich, Switzerland.
Arch Insect Biochem Physiol (UNITED STATES) 1997, 35 (1-2) p59-69, ISSN 0739-4462 Journal Code: A9G
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The functional ecdysteroid receptor complex consists of a nuclear receptor heterodimer of ecdysteroid receptor (EcR) and ultraspiracle (USP). EcR and USP of both Chironomus tentans and Drosophila melanogaster were expressed in Escherichia coli as fusion proteins with glutathione S-transferase (GST). Cell lysis and protein solubilization with the **anionic detergent sarkosyl** yielded preparations of EcR and USP with properties similar to those of the endogenous receptors in various respects. The heterodimer of the expressed proteins specifically bound the labeled ecdysteroid (Ec) [3H]ponasterone A. Furthermore, it preferentially recognized the palindromic ecdysone response element (EcRE) PALI. Interestingly, binding to the PAL1 element was also observed for EcR homodimers. USP homodimers, in turn, preferentially bound to the direct repeat element DR1. When incubated with native polytene chromosomes of Chironomus, EcR/USP specifically accumulated at the early Ec-inducible puff site IV-2B.

3/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09021837 97219982
Retinoid X receptor:vitamin D3 receptor heterodimers promote stable preinitiation complex formation and direct 1,25-dihydroxyvitamin D3-dependent cell-free transcription.
Lemon BD; Fondell JD; Freedman LP
Molecular Biology Program, Memorial Sloan-Kettering Cancer Center, Cornell University Graduate School of Medical Sciences, New York, New York 10021, USA.
Mol Cell Biol (UNITED STATES) Apr 1997, 17 (4) p1923-37, ISSN 0270-7306 Journal Code: NGY
Contract/Grant No.: DK45460, DK, NIDDK; CA08748, CA, NCI; CA09182, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The numerous members of the steroid/nuclear hormone receptor superfamily act as direct transducers of circulating signals, such as steroids, thyroid hormone, and vitamin or lipid metabolites, and modulate the transcription of specific target genes, primarily as dimeric complexes. The receptors for 9-cis retinoic acid and 1,25-dihydroxyvitamin D3 [1,25(OH)2D3], RXR and VDR, respectively, as members of this superfamily, form a heterodimeric complex and bind cooperatively to vitamin D responsive elements (VDREs) to activate or repress the transcription of a multitude of genes which regulate a variety of physiological functions. To directly investigate RXR- and VDR-mediated transactivation, we developed a cell-free transcription system for 1,25(OH)2D3 signaling by utilizing crude nuclear extracts and a

dependent on purified, [redacted]ogenous RXR and VDR and w[redacted] responsive to physiological concentrations of 1,25(OH)2D3. We found that RXR and VDR transactivated selectively from VDRE-linked templates exclusively as a heterodimeric complex, since neither receptor alone enhanced transcription in vitro. By the addition of low concentrations of the **anionic detergent Sarkosyl** to limit cell-free transcription to a single round and the use of agarose gel mobility shift experiments to assay factor complex assembly, we observed that 1,25(OH)2D3 enhanced RXR:VDR-mediated stabilization or assembly of preinitiation complexes to effect transcriptional enhancement from VDRE-linked promoter-containing DNA.

3/3,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08689902 96221291
Distinct effects of ATP on transcription complex formation and initiation in a yeast in vitro transcription system.
Coda-Zabetta F; Boam DS
School of Biological Sciences, University of Manchester, UK.
Biochim Biophys Acta (NETHERLANDS) May 2 1996, 1306 (2-3) p194-202, ISSN 0006-3002 Journal Code: A0W
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The stages and kinetics of transcription complex formation in a Saccharomyces cerevisiae in vitro transcription system were analysed using the **anionic detergent sarkosyl**. In contrast to findings from other systems, we were not able to distinguish between a fully formed pre-initiation complex and a 'rapid start' complex to which nucleotides were added. A further increase in resistance of transcription to **sarkosyl** was only observed 12 min after transcription initiation, by which time elongation was underway. Low concentrations of ATP, dATP or, surprisingly, the non-hydrolysable analogue ATPgammaS selectively stimulated transcription when present during assembly of transcription complexes, although the level of stimulation dropped when ATP was added progressively later. The effect of ATP did not correlate with the kinetics of template commitment, signifying that it functioned at a later stage than this, but prior to the full assembly of **sarkosyl** -resistant pre-initiation complexes. ATP also altered the **sarkosyl** resistance of initiating transcription complexes possibly by affecting a rate-limiting step leading to earlier appearance of elongated transcripts. This effect was antagonised by ATPgammaS, thus providing evidence that the stimulatory effect of ATP on pre-initiation complex formation and its effect on the lag between initiation and elongation phases are distinct.

3/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08487068 96070916
Oct-1 protein promotes functional transcription complex assembly on the mouse mammary tumor virus promoter.
Kim MH; Peterson DO
Department of Biochemistry and Biophysics, Texas A & M University, College Station 77843-2128, USA.
J Biol Chem (UNITED STATES) Nov 17 1995, 270 (46) p27823-8, ISSN 0021-9258 Journal Code: HIV
Contract/Grant No.: CA32695, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The ubiquitous transcription factor Oct-1 stimulates basal transcription from the mouse mammary tumor virus (MMTV) promoter by binding to

mechanism of transcripti[redacted]l activation by Oct-1 was inve[redacted]gated using in vitro transcription assays with a HeLa cell nuclear extract depleted of endogenous Oct-1. Oct-1-mediated transcriptional activation could be reconstituted by addition of bacterially expressed recombinant Oct-1 protein. The stimulatory effect of Oct-1 was observed only when the protein was present during formation of transcription preinitiation complexes and not when added to fully assembled complexes. Furthermore, assembled MMTV preinitiation complexes were resistant to inhibition by a competitor oligonucleotide containing MMTV octamer-related elements that could eliminate Oct-1-mediated stimulation when present during the assembly process. The time course of transcription complex assembly revealed that Oct-1 increases the number of templates on which functional transcription complexes form. Finally, experiments designed to exploit the sensitivity of discrete steps in transcription complex assembly to the **anionic detergent Sarkosyl** demonstrated that Oct-1 must be present during formation of an early intermediate in the assembly process.

3/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08416349 95164518
Architecture of the cell envelope of Chlamydia psittaci 6BC.
Everett KD; Hatch TP
Department of Microbiology and Immunology, University of Tennessee, Memphis 38163.
J Bacteriol (UNITED STATES) Feb 1995, 177 (4) p877-82, ISSN 0021-9193 Journal Code: HH3
Contract/Grant No.: AI19570, AI, NIAID
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The cysteine-rich envelope proteins of the elementary body form of chlamydiae are thought to be located in the outer membrane on the basis of their insolubility in the weak **anionic detergent** N-lauryl sarcosinate (**Sarkosyl**). We found, however, that the insolubility of the small (EnvA) and the large (EnvB) cysteine-rich proteins of Chlamydia psittaci 6BC in **Sarkosyl** is dependent on the maintenance of a supramolecular disulfide-cross-linked complex and is unlikely to be a valid indicator of outer membrane location. Consequently, we used other methods to characterize the architecture of the cell envelope of C. psittaci 6BC. We found that disulfide-reduced EnvA, previously shown to be a lipoprotein, segregated into the **detergent** phase during Triton X-114 partitioning experiments and was recovered from the membrane fraction of elementary bodies lysed by nondetergent means. In contrast, disulfide-reduced EnvB segregated to the aqueous phase in partitioning experiments and was found in the soluble fraction of elementary bodies lysed in the absence of detergents. The hydrophobic affinity probe 3-(trifluoromethyl)-3-(m-[125I]iodophenyl)-diazirine labeled the major outer membrane protein and EnvA but did not label EnvB. Treatment of intact elementary bodies of C. psittaci with trypsin had no effect on the cysteine-rich proteins, although the major outer membrane protein was partially degraded. On the basis of these and other observations, we propose that EnvA is anchored to the outer membrane by its lipid moiety, with a hydrophilic peptide portion extending into the periplasm, and that EnvB is located exclusively within the periplasm. We further propose that disulfide-cross-linked polymers of EnvB are the functional equivalent of peptidoglycan, forming a disulfide-cross-linked network with the periplasmic domains of EnvA and other membrane proteins, which accounts for the osmotic stability of elementary bodies.

3/3,AB/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08172297 95040248
Characterization of a serum factor that decreases albumin mRNA in cultured hepatocytes.
Johnston DE; Jefferson DM
Department of Medicine, New England Medical Center, Boston, Massachusetts 02111.
In Vitro Cell Dev Biol Anim (UNITED STATES) Jul 1994, 30A (7) p464-70, ISSN 1071-2690 Journal Code: BZE
Contract/Grant No.: NIDDKD P30 AM34928, AM, NIADDK; T32 AM07024, AM, NIADDK; R29 DK 42161, DK, NIDDK
Languages: ENGLISH
Document type: JOURNAL ARTICLE
When primary cultures of hepatocytes are exposed to media containing fetal bovine serum (FBS) there is a rapid decrease in levels of tissue-specific mRNAs such as albumin mRNA. We used Northern blot analysis to examine mRNA levels in cultured hepatocytes, and characterized the factor in FBS that significantly reduces the steady state albumin mRNA level. Neonatal bovine serum or serum derived from platelet-poor calf plasma proved as potent as did FBS, but commercial bovine serum albumin did not exhibit this inhibitory activity. Inhibitory activity of FBS was not removed by moderate heat treatment, dialysis, or extraction with organic solvents. However, incubation of FBS with a highly **anionic detergent** such as 0.1% sodium dodecyl sulfate or N-lauroyl sarcosine, followed by extensive dialysis, resulted in sera that did not inhibit expression of albumin mRNA. These sera supported cell attachment and seemed non-toxic toward the cells. Ammonium sulfate fractionation of FBS showed the activity was present in the 45 to 70% fraction, and trypsin digestion destroyed the inhibitory activity. Gel exclusion chromatography gave a molecular weight of 60,000 to 70,000. Fractionation of serum proteins by DEAE-Sephacel or Cibacron blue-agarose showed enrichment for albumin in the most active fractions. Interestingly, metabolic labeling of secreted and cellular proteins with 35S-methionine and cysteine showed no significant difference between hepatocytes maintained for 2 days beforehand in serum-free or serum-supplemented media, and no difference between **detergent** -treated FBS and control FBS.(ABSTRACT TRUNCATED AT 250 WORDS)

3/3,AB/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06424282 90320147
In vitro regulation of human hepatitis B virus core gene transcription.
Waisman A; Aloni Y; Laub O
Department of Molecular Genetics and Virology, Weizmann Institute of Science, Rehovot, Israel.
Virology (UNITED STATES) Aug 1990, 177 (2) p737-44, ISSN 0042-6822 Journal Code: XEA
Contract/Grant No.: CA 14995, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
In the present study we used a HeLa whole cell extract transcription system to map the transcription start sites and the minimal promoter of the hepatitis B virus core gene. Two initiation sites located at residues 1792 +/- 5 and 1817 +/- 5 were identified. The minimal upstream region essential and sufficient for transcription was defined to a 105-base pair DNA fragment. These results are identical to the in vivo mapping of the transcription start sites and the minimal core gene promoter. When in vitro transcription elongation was carried out in the presence of the **anionic detergent Sarkosyl** , known to enhance premature transcription termination (attenuation), two short transcripts (as well as two run-offs) were synthesized. Kinetic studies indicated that the short

RNA processing. RNA ma[redacted]ng showed that the short atten[redacted]ed transcripts indeed initiated at the two core gene initiation sites and both prematurely terminated at nucleotide 1966 +/- 5, defined as the attenuation site. This site is located in the attenuator RNA within a uridine-rich sequence preceded by a stable hairpin structure. Attenuation at the same site occurred when transcription of the core gene was directed by the Ad2 major late promoter (MLP) and when the poly(A) signal, which precedes the attenuation site, was mutated from TATAAA to TAGAAA. We suggest that the elongation block at nt 1966 +/- 5 in vivo exerts a dual function: first, it regulates the level of RNA by attenuation during the first cycle of transcription and, second, it acts as a termination site at the end of the primary RNA transcript.

3/3,AB/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06406090 90277695
Solubilization of the 97-kDa native form of liver microsomal 3-hydroxy-3-methylglutaryl-coenzyme A reductase.
Vermilion JL; Schroepfer GJ Jr
Department of Biochemistry and Cell Biology, Rice University, Houston, Texas 77251-1892.
J Biol Chem (UNITED STATES) Jun 15 1990, 265 (17) p9984-92, ISSN 0021-9258 Journal Code: HIV
Contract/Grant No.: HL-15376, HL, NHLBI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Liver microsomal 3-hydroxy-3-methylglutaryl-CoA reductase was partially purified from cholestyramine-fed rats by sequential extraction of the membrane with 3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulfonate (CHAPS) and polyethylene glycol nonylphenyl ether (Triton N-101) and solubilized by incorporation of the resulting insoluble protein preparation into a **detergent** mixture of Triton N-101 and sodium N-lauroylsarcosinate (**Sarkosyl**) in the presence of high salt. The purification procedure resulted in approximately a 3-4-fold increase in specific activity compared with the microsomal fraction, and the enzyme was recovered with yields as high as 63%. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis and a blotting experiment using antiserum to the purified 53,000-dalton reductase fragment showed that the major immunoreactive polypeptide had a Mr of 97,000, that expected for the native intact form of the enzyme (Chin, D. J., Gil, G., Russell, D. W., Liscum, L., Luskey, K. L., Basu, S. K., Okayama, H., Berg, P., Goldstein, J. L., and Brown, M. S. (1984) Nature 308, 613-617). In addition, the effect of various detergents on the activity and stability of the membrane-bound and the partially purified enzyme was determined, and a method for protection of the reductase from inactivation caused by the addition of **anionic** detergents to the assay mixture is described.

3/3,AB/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04360349 81218447
Two deletions within genes for simian virus 40 structural proteins VP2 and VP3 lead to formation of abnormal transcriptional complexes.
Llopis R; Stark GR
J Virol (UNITED STATES) Apr 1981, 38 (1) p91-103, ISSN 0022-538X Journal Code: KCV
Contract/Grant No.: CA17287, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE

29:612-623, 1979) for i[redacted]ating simian virus 40 (SV 40) [redacted]omatin free of disrupted previrions was optimized for preparing late transcriptional complexes, and these complexes were partially characterized. Transcriptional complexes derived from wild-type virus and from several deletion and temperature-sensitive mutants could be activated more than five-fold either by the **anionic detergent Sarkosyl** or by 300 mM ammonium sulfate, in agreement with the properties of SV40 transcriptional complexes prepared by other procedures. In contrast, complexes from cells infected with deletion mutants dl1261 or dl1262 were not activated at all by a high salt concentration, even though the extent of their activation by **Sarkosyl** was normal. Mutants dl1261 and dl1262 carry deletions of 54 and 36 base pairs, respectively, at an approximate map position of 0.91, which is within the overlapping genes for the virion proteins VP2 and VP3. The effects of these deletions on transcription in vitro indicate that VP2 or VP3 or both are bound to late transcriptional complexes in a way that affects the progress of initiated RNA polymerase. The properties of late transcriptional complexes derived from wild-type SV40 can be explained by the presence of the following two different kinds of complexes: (i) a minority class (about 20%), which is free of VP2 or VP3, active at low concentrations of ammonium sulfate in vitro, and responsible for late transcription in vivo, and (ii) a majority class (about 80%) with VP2 or VP3 bound, which is inactive at low salt concentrations both in vitro and in vivo but capable of being activated by high salt concentrations or by **Sarkosyl**. We propose that mutant VP2 and VP3 proteins from dl1261 and dl1262 bind to the majority class of late transcriptional complexes in a way that can be reversed by **Sarkosyl** but not by a high salt concentration.

3/3,AB/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03413604 81191028

Purification and partial characterization of the major outer membrane protein of Chlamydia trachomatis.

Caldwell HD; Kromhout J; Schachter J

Infect Immun (UNITED STATES) Mar 1981, 31 (3) p1161-76, ISSN 0019-9567 Journal Code: GO7

Contract/Grant No.: EY 03046, EY, NEI; EY 01198, EY, NEI; EY 02216, EY, NEI; +

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Elementary bodies (EB) of Chlamydia trachomatis serotypes C, E, and L2 were extrinsically radioiodinated, and whole-cell lysates of these serotypes were compared by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE). Autoradiography of the polypeptide profiles identified a major surface protein with an apparent subunit molecular weight of 39,500 that was common to each C. trachomatis serotype. The abilities of nonionic (Triton X-100), dipolar ionic (Zwittergent TM-314), mild (sodium deoxycholate and sodium N-lauroyl sarcosine), and strongly **anionic** (SDS) detergents to extract this protein from intact EB of the L2 serotype were investigated by SDS-PAGE analysis of the soluble and insoluble fractions obtained after each **detergent** treatment. Only SDS readily extracted this protein from intact EB. **Sarkosyl** treatment selectively solubilized the majority of other EB proteins, leaving the 39,500-dalton protein associated with the **Sarkosyl** -insoluble fraction. Ultrastructural studies of the **Sarkosyl**-insoluble EB pellet showed it to consist of empty EB particles possessing an apparently intact outer membrane. No structural evidence for a peptidoglycan-like cell wall was found. Morphologically these chlamydial outer membrane complexes (COMC) resembled intact chlamydial EB outer membranes. The 39,500-dalton outer membrane protein was quantitatively extracted from COMC by treating them with 2% SDS at 60 degrees C. This protein accounted for 61% of the total

of the COMC membrane stru[redacted]re and morphology. The soluble [redacted]tract obtained from SDS-treated COMC was adsorbed to a hydroxylapatite column and eluted with a linear sodium phosphate gradient. The 39,500-dalton protein was eluted from the column as a single peak at a phosphate concentration of approximately 0.3 M. The eluted protein was nearly homogeneous by SDS-PAGE and appeared free of contaminating carbohydrate, glycolipid, and nucleic acid. Hyperimmune mouse antiserum prepared against the 39,500-dalton protein from serotype L2 reacted with C. trachomatis serotypes Ba, E, D, K, L1, L2, and L3 by indirect immunofluorescence with EB but failed to react with serotypes A, B, C, F, G, H, I, and J, with the C. trachomatis mouse pneumonitis strain, or with the C. psittaci feline pneumonitis, guinea pig inclusion conjunctivitis, or 6BC strains. Thus, the 39,500-dalton major outer membrane protein is a serogroup antigen of C. trachomatis organisms.

3/3,AB/12 (Item 12 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03211047 77004059
Effect of **Sarkosyl** on chromatin and viral RNA synthesis. The isolation of SV40 transcription complex.
Gariglio P
Differentiation (ENGLAND) Jun 4 1976, 5 (2-3) p179-83, ISSN 0301-4681 Journal Code: E99
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The endogenous RNA polymerase activity of mouse nucleic is enhanced several-fold by the **anionic detergent Sarkosyl** . The action of **Sarkosyl** is exerted primarily on the alpha-amanitin sensitive form of the enzyme. This **detergent** causes the release of nearly all the protein associated with cellular DNA but does not release initiated RNA polymerase. **Sarkosyl** was also able to activate the RNA polymerase activity from mitotic cells, in which transcription of the highly condensed chromatin is minimal. The use of this **anionic detergent** has also permitted the extraction of a nucleoprotein complex from Simian Virus 40 (SV40) infected monkey cells. Molecular hybridization experiments have established the viral specificity of the RNA synthesized in vitro by the endogenous polymerase present in this complex.

3/3,AB/13 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03048468 79007617
Characterization of a DNA-protein complex and capsomere subunits derived from polyoma virus by treatment with ethyleneglycol-bis-N,N'-tetraacetic acid and dithiothreitol.
Brady JN; Winston VD; Consigli RA
J Virol (UNITED STATES) Jul 1978, 27 (1) p193-204, ISSN 0022-538X Journal Code: KCV
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Treatment of polyoma virions with ethyleneglycol-bil-N,N'-tetraacetic acid (EGTA) and dithiothreitol (DTT) at pH 8.5 resulted in the dissociation of the virions into a DNA-protein complex and individual structural capsomere subunits. The sedimentation value of the DNA-protein complex in sucrose gradients was approximately 48S, and it had a density of 1.45 g/cm3 in equilibrium CsCl gradients. Alkaline sucrose analysis of the DNA within this DNA-protein complex demonstrated that approximately 75% of the DNA is component 1. The proteins associated with the DNA were dissociated by treatment with either NaCl or the **anionic detergent Sarkosyl** . VP1 and the histone proteins VP 4--7 were the major

alkaline pH resulted in t[redacted]specific removal of FP1. Elect[redacted] microscopy of the 48S DNA-protein complex demonstrated that it is a ve[redacted] tightly coiled structure that is slightly larger than the intact virion. Treatment of the complex with either NaCl or with pH 10.5 buffer resulted in the loss of protein and subsequent loosening of the DNA-protein complex such that the DNA could be visualized. The capsomere subunits released as a result of the EGTA-DTT treatment sedimented as 18S, 12S, and 5S subunits in sucrose gradients. Electrophoretic analysis of the isolated capsomeres demonstrated that VP1, VP2, and VP3 were present in each species, although the ratios of the proteins varied. In addition to the structural proteins, histones VP 4--7 were found to be predominantly associated with the 5S capsomere subunit.

3/3,AB/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02563808 79000587
Solubilization of Spiroplasma citri cell membrane proteins with the **anionic detergent** sodium lauroyl-sarcosinate (**Sarkosyl**).
Wroblewski H; Burlot R; Johansson KE
Biochimie (FRANCE) 1978, 60 (4) p389-98, ISSN 0300-9084
Journal Code: A14
Languages: ENGLISH
Document type: JOURNAL ARTICLE
1. Up to 90 per cent of the membrane proteins from Spiroplasma citri could be solubilized with the **anionic detergent Sarkosyl** (sodium lauroyl-sarcosinate). Maximal solubilization was obtained with 6 to 20 mumoles of of **detergent** per mg of membrane protein. The insoluble residue, comprising about 10 per cent of the membrane protein, contained mainly the protein spiralin, which is quantitatively the major one of this membrane. 2. Mg2+ ions completely prevented solubilization of the membrane proteins at a molar ratio of MgCl2/**Sarkosyl** greater than 0.5. 3. The selectivity of **Sarkosyl** was also tested at low **detergent** concentrations and in the presence of Mg2+ ions. Spiralin was the least soluble protein also under these conditions. Other proteins were not selectively solubilized. 4. An electrophoretical and immunoelectrophoretical approach was used to study the interaction between **Sarkosyl** and membrane proteins. The results indicated that **Sarkosyl** should be considered as a mild **detergent** which usually solubilizes membrane proteins without gross donformational changes. This hypothesis was supported by experiments with a membrane-bound enzyme in the presence of **Sarkosyl**.

3/3,AB/15 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

03671923 BIOSIS NO.: 000074087500
EFFECTS OF DETERGENTS AND DIVALENT CATIONS ON THE FUNCTIONING OF CELL ENVELOPES OF ESCHERICHIA-COLI IN THE EARLY STAGES OF INFECTION WITH BACTERIO PHAGE PHI-X-174
AUTHOR: MANO Y; KAWABE T; OBATA K; YOSHIMURA T; KOMANO T
AUTHOR ADDRESS: LABORATORY BIOCHEMISTRY, DEP. AGRICULTURAL CHEMISTRY, KYOTO UNIV., KYOTO 606, JPN.
JOURNAL: AGRIC BIOL CHEM 46 (3). 1982. 631-638.
FULL JOURNAL NAME: Agricultural and Biological Chemistry
CODEN: ABCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Effects of detergents and divalent cations (Ca2+, Mg2+) on intact

eclipse kinetics of bac[redacted]iophage .vphi.X174 and by poly[redacted]ylamide gel electrophoresis of cell envelope proteins. Cell envelopes having receptor activity to convert .vphi.X174 to eclipsed particles (eclipsing activity) were destroyed by cationic **detergent** cetyl trimethyl ammonium bromide (CTAB) and **anionic detergent** N-lauroyl sarcosine sodium salt (**Sarkosyl**), but were not destroyed by many nonionic detergents, such as Triton X-100, Pluronic P103, Brij 58, Tween 20 and Tween 80 in the presence of divalent cations. Nonionic **detergent** Span 80 caused the disruption of cell envelopes in the presence of a low concentration (1 mM) of divalent cations, but not in the presence of a higher concentration (5 mM) of divalent cations. Divalent cations were shown to stabilize the cell envelope structure and to protect the cell envelopes from solubilization by detergents.

3/3,AB/16 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

03584374 BIOSIS NO.: 000073087455
DNA BOUND RNA POLYMERASES DURING POLIOVIRUS INFECTION REDUCTION IN THE NUMBER OF FORM II ENZYME MOLECULES
AUTHOR: FLORES-OTERO G; FERNANDEZ-TOMAS C; GARIGLIO-VIDAL P
AUTHOR ADDRESS: DEP. DE GENETICA AND BIOL. MOLECULAR, CENTRO DE INVESTIGACION AND ESTUDIOS AVANZADOS DEL IPN, APARTADO POSTAL 14-740, MEXICO CITY, MEXICO.
JOURNAL: VIROLOGY 116 (2). 1982. 619-628.
FULL JOURNAL NAME: Virology
CODEN: VIRLA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The **anionic detergent Sarkosyl**, known to dissociate most of the proteins from chromatin, was employed to determine the relative number of chromatin-bound RNA polymerases at different times of poliovirus infection. Both this approach and one using a coupled strategy employing **Sarkosyl** and 32P-labeled cordycepin indicate that the number of polymerase II molecules engaged in chain elongation decreases as infection proceeds. At 2 h after polio infection, the irreversible inhibition of RNA polymerase II parallels the appearance of a viral-induced polypeptide in the nuclei of infected cells. The possibility that the inhibition may occur at the level of chain initiation is discussed. [Human cervical carcinoma HeLa cells were used in this study.]

3/3,AB/17 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

03316984 BIOSIS NO.: 000072045088
2 DELETIONS WITHIN GENES FOR SV-40 STRUCTURAL PROTEINS VP-2 AND VP-3 LEAD TO FORMATION OF ABNORMAL TRANSCRIPTIONAL COMPLEXES
AUTHOR: LLOPIS R; STARK G R
AUTHOR ADDRESS: DEP. OF BIOCHEM., STANFORD UNIV. SCH. OF MED., STANFORD, CALIF. 94305.
JOURNAL: J VIROL 38 (1). 1981. 91-103.
FULL JOURNAL NAME: Journal of Virology
CODEN: JOVIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The procedure developed by R. M. Fernandez-Munoz et al. for isolating SV40 chromatin free of disrupted previrions was optimized for

preparing late transcriptional complexes [from SV40 infected [redacted] green monkey kidney CV1 [redacted] cells]; these complexes were partially characterized. Transcriptional complexes derived from wild-type virus and from several deletion and temperature-sensitive mutants could be activated > 5-fold either by the **anionic detergent** **Sarkosyl** or by 300 mM ammonium sulfate, in agreement with the properties of SV40 transcriptional complexes prepared by other procedures. Complexes from cells infected with deletion mutants dl1261 or dl1262 were not activated at all by a high salt concentration, even though the extent of their activation by **Sarkosyl** was normal. Mutants dl1261 and dl1262 carry deletions of 54 and 36 base pairs, respectively, at an approximate map position of 0.91, which is within the overlapping genes for the virion proteins VP2 and VP3. The effects of these deletions on transcription in vitro indicate the VP2 or VP3 or both are bound to late transcriptional complexes in a way that affects the progress of initiated RNA polymerase. The properties of late transcriptional complexes derived from wild-type SV40 can be explained by the presence of the following 2 different kinds of complexes: a minority class (.apprx. 20%), which is free of VP2 or VP3, active at low concentrations of ammonium sulfate in vitro and responsible for late transcription in vivo; and a majority class (.apprx. 80%) with VP2 or VP3 bound, which is inactive at low salt concentrations in vitro in vivo but capable of being activated by high salt concentrations or by **Sarkosyl**. Mutant VP2 and VP3 proteins from dl1261 and dl1262 may bind to the majority class of late transcriptional complexes in a way that can be reversed by **Sarkosyl** but not by a high salt concentration.

3/3,AB/18 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02762503 BIOSIS NO.: 000068073112
COMPARATIVE STUDY OF CALF THYMUS AND WHEAT GERM RNA POLYMERASE II STABILITY OF INITIATION COMPLEXES AND ELONGATION RATES
AUTHOR: SARAGOSTI S; LESCURE B; YANIV M
AUTHOR ADDRESS: DEP. MOL. BIOL., INST. PASTEUR, 75015 PARIS, FR.
JOURNAL: BIOCHEM BIOPHYS RES COMMUN 88 (3). 1979. 1077-1084.
FULL JOURNAL NAME: Biochemical and Biophysical Research Communications
CODEN: BBRCA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Pure wheat germ RNA polymerase II but not calf thymus RNA polymerase II forms relatively stable binary complexes (half-life 30 min. at 0.degree. C) with superhelical SV 40 DNA. The addition of a specific dinucleotide and a single ribotriphosphate permits the formation of highly stable complexes between both enzymes and SV 40 DNA. Once initiated, the elongation of RNA chains is stimulated by **sarkosyl** (an **anionic detergent**) only in the case of the wheat germ enzyme. The wheat germ enzyme, compared with the calf thymus enzyme, may contain a protein factor and/or a more native structure that permits efficient initiation and elongation of RNA chains on double stranded DNA.

3/3,AB/19 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02619678 BIOSIS NO.: 000067007736
TEMPLATE ENGAGED AND FREE RNA POLYMERASES DURING XENOPUS-LAEVIS ERYTHROID CELL MATURATION
AUTHOR: HENTSCHEL C C; TATA J R
AUTHOR ADDRESS: NATL. INST. MED. RES., MILL HILL, LONDON NW7 1AA, ENGL.,

JOURNAL: DEV BIOL 65 (2). 78 496-507.
FULL JOURNAL NAME: Developmental Biology
CODEN: DEBIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Free and template-engaged RNA polymerase activities were measured in nuclei from mature and from different stages of developing X. laevis erythroid cells. Immature erythroid cell nuclei were significantly more active in RNA synthesis than mature erythrocyte nuclei and contain both .alpha.-amanitin-sensitive (RNA polymerase II) and -insensitive (RNA polymerase I and III) activities. Transcriptionally inactive mature erythrocyte nuclei retain only RNA polymerase II activity predominantly present as engaged transcription complexes but with a restricted ability to elongate RNA chains in vitro. The **anionic detergent Sarkosyl** greatly stimulates this activity in the same concentration range required to solubilize the majority of chromatin-bound protiens (principally histones) from these highly condensed nuclei. Quantitation of relative numbers of RNA chains synthesized in the presence and absence of **Sarkosyl** reveals that this stimulation results from an increase in average RNA chain elongation rate and not from activation of a silent RNA polymerase population. Significance of the retention of RNA polymerase II transcription complexes in the transcriptionally inactive,

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? s non ionic detergent and py<1997

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             0  NON IONIC DETERGENT
      19720586  PY<1997
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       2919998  NON
         74297  IONIC
         42130  DETERGENT
          1689  NON(W)IONIC(W)DETERGENT
      19720586  PY<1997
      S2  1487  NON (W) IONIC (W) DETERGENT AND PY<1997
? s s2 and sarkosyl

          1487  S2
           835  SARKOSYL
      S3    2  S2 AND SARKOSYL
? rd

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      S4    1  RD (unique items)
? t s4/3,ab/all


 4/3,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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04036341   84269063
  Nuclear androgen binding sites in the male rat. III. Late spermatids and
spermatozoa in the testis, with an introduction to epididymal spermatozoa.
  Frankel AI; Chapman JC
  Journal of steroid biochemistry (ENGLAND)  Jun 1984,  20 (6A)
p1301-11, ISSN 0022-4731  Journal Code: K70
  Contract/Grant No.:  AG-01155,  AG,  NIA;  HD-04081,  HD,  NICHD;
S07-RR-07149-10, RR, NCRR
  Languages: ENGLISH
  Document type: JOURNAL ARTICLE
  Nuclear androgen binding sites were examined in late spermatids (stages
12-19) which resisted sonication of homogenized testes of mature male rats.
The measurement of unoccupied binding sites in salt extract of purified
spermatid heads by nuclear exchange at -10 degrees C was developed and
validated. As in the prostate, unoccupied nuclear androgen binding sites in
sonicated testes were in low concentration, were not artefactual, and could
be occupied both in vivo and in vitro by exogenous androgens, and uniquely
in hemicastrated rats by endogenously compensated androgens in the
remaining testis. The properties of occupied binding sites in salt extract
of purified spermatid heads (measured by nuclear exchange at 4 degrees C
for 48 or more hours with 5 nM [3H]dihydrotestosterone) were almost
identical to those of occupied binding sites in nuclei of the ventral
prostate, except for their concentration. However, levels of specific
binding activity approaching 50 fmol/mg DNA could be expected in salt
extract of spermatid pellets, by use of a sulfhydryl reducing agent
(dithiothreitol) prior to salt extraction, a protease inhibitor
(phenylmethylsulfonyl fluoride) in all buffers, and optimization of the
sonication protocol. Nuclear androgen binding sites of sonicated epididymal
spermatozoa, collected by retrograde perfusion of the cauda epididymidis,
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were found to be completely salt-resistant. These binding proteins could be extracted by 0.4 M KCl if dithiothreitol and dihydrotestosterone were incorporated into the sonication buffer, if phenylmethylsulfonyl fluoride was added to all buffers, and if the purified epididymal sperm pellet was treated with **sarkosyl**, a **non-ionic detergent**, just before salt extraction. The salt extract of epididymal spermatozoa which were treated as described above contained two binding components: a soluble form which was eluted from hydroxylapatite by increasing concentrations of phosphate buffers, and a non-soluble form, free of DNA, which remained in the hydroxylapatite column, and which contained most of the androgen binding sites. Affinity (Kd) of dihydrotestosterone to the soluble and insoluble fractions of the steroid-binding protein complex was determined to be 0.7 and 0.1 nM, respectively. Salt-resistance of binding proteins in germ cells was shown to develop significantly in the last stages of

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 s s2 and rna (w) extract?

           1487  S2
         618100  RNA
         510535  EXTRACT?
           4581  RNA(W)EXTRACT?
     S5       2  S2 AND RNA (W) EXTRACT?
? rd

...completed examining records
     S6       1  RD (unique items)
? t s6/3,ab/all


 6/3,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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07879657   94155897
  Purification, characterization and molecular cloning of human hepatic
lysosomal acid lipase.
  Ameis D; Merkel M; Eckerskorn C; Greten H
  Department of Medicine, University Hospital Eppendorf, Hamburg, Germany.
  European journal of biochemistry (GERMANY)  Feb 1 1994,  219 (3)
p905-14,  ISSN 0014-2956  Journal Code: EMZ
  Languages: ENGLISH
  Document type: JOURNAL ARTICLE
  Lysosomal acid lipase (LAL) is a hydrolase essential for the
intracellular degradation of cholesteryl esters and triacylglycerols. This
report describes a multi-step procedure for the purification of LAL from
human liver. After solubilization with non-ionic
detergent , acid hydrolase activity was purified 17000-fold to
apparent homogeneity by sequential chromatography on Concanavalin A
Sepharose, carboxymethyl-cellulose, phenyl Superose, Mono S cation exchange
and Superose 12 gel-filtration columns. This procedure yielded two
silver-staining protein bands of 56 kDa and 41 kDa on SDS/PAGE.
Size-exclusion chromatography of the 41-kDa protein indicated that the
enzyme was catalytically competent as a monomer of approximately 38 kDa.
When assayed in the presence of cholesteryl oleate or trioleoylglycerol,
purified acid lipase had Vmax values of 4390 nmol fatty acid.min-1.mg
protein and 4756 nmol fatty acid.min-1.mg protein-1, and apparent Km values
of 0.142 mM and 0.138 mM, respectively. The purified enzyme was most active
at low pH (4.5-5.0) and required non-ionic detergent and
ethylene glycol for optimal stability. Incubation of the 41-kDa acid lipase
with endoglucosaminidase H reduced the molecular mass by 4-6 kDa,
demonstrating Asn-linked glycosylation with high-mannose oligosaccharides.
Deglycosylation did not affect enzymic activity, indicating that
carbohydrates are not required for LAL activity. Based on partial peptide
sequence, an oligonucleotide was synthesized and utilized to isolate LAL
cDNA clones from a human liver cDNA library. A full-length LAL cDNA
contained 2626 nucleotides and coded for a predicted protein of 372 amino
acids, preceded by a 27 residue hydrophobic signal peptide. Hepatic LAL
differed from fibroblast acid lipase at the N-terminus and revealed
extensive similarities with human gastric lipase and rat lingual lipase,
confirming a gene family of acid lipases. Northern hybridization using the
complete LAL cDNA as a radiolabeled probe indicated striking differences in
mRNA expression among human tissues. LAL mRNA was most abundant in brain,
lung, kidney and mammary gland. Placenta and HeLa cells expressed
intermediate amounts of LAL mRNA, while RNA extracted from
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liver and heart showed low levels of expression.
? s s2 and rna

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          1487  S2
        618100  RNA
     S7      79  S2 AND RNA
? rd

...examined 50 records  (50)
...completed examining records
     S8      63  RD (unique items)
? t s8/3,ab/all
```

8/3,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08707814 96181348
Phragmoplastin, a dynamin-like protein associated with cell plate formation in plants.
Gu X; Verma DP
Department of Molecular Genetics, Ohio State University, Columbus, 43210, USA.
EMBO journal (ENGLAND) Feb 15 **1996**, 15 (4) p695-704, ISSN 0261-4189 Journal Code: EMB
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Cytokinesis in a plant cell is accomplished by the formation of a cell plate in the center of the phragmoplast. Little is known of the molecular events associated with this process. In this study, we report the identification of a dynamin-like protein from soybean and demonstrate that this protein is associated with the formation of the cell plate. Plant dynamin-like (PDL) protein contains 610 amino acids showing high homology with other members of the dynamin protein family. Western blot experiments demonstrated that it is associated with the **non-ionic detergent** -resistant fraction of membranes. Indirect immunofluorescence microscopy localized PDL to the cell plate in dividing soybean root tip cells. Double labeling experiments demonstrated that, unlike phragmoplast microtubules which are concentrated on the periphery of the forming plate, PDL is located across the whole width of the newly formed cell plate. Based on the temporal and spatial organization of PDL in the phragmoplast, we termed this protein 'phragmoplastin'. The data suggest that phragmoplastin may be associated with exocytic vesicles that are depositing cell plate material during cytokinesis in the plant cell.

8/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08461344 96049890
Abnormal A-type lamin organization in a human lung carcinoma cell line.
Machiels BM; Broers JL; Raymond Y; de Ley L; Kuijpers HJ; Caberg NE; Ramaekers FC
Department of Molecular Cell Biology & Genetics, University of Limburg, Maastricht, The Netherlands.
European journal of cell biology (GERMANY) Aug **1995**, 67 (4) p328-35, ISSN 0171-9335 Journal Code: EM7
Languages: ENGLISH
Document type: JOURNAL ARTICLE
We have studied the expression of lamins A and C (A-type lamins) in a lung carcinoma cell line using type-specific monoclonal antibodies. Using immunofluorescence and immunoblotting studies it was noted that several irregularities in lamin expression exist in the cell line GLC-A1, derived

from an adenocarcinoma. First, the expression of the A-type lamins was lower than in other adenocarcinoma cell lines of the lung. Also the ratio between lamins A and C proteins was 1:8 instead of the 1:1 ratio seen in the other cell lines. Northern blotting confirmed the altered level of A-type lamin expression. Secondly, an abnormal localization of lamin A was observed. Intensely fluorescing lamin A aggregates were observed in the nucleus, rather than the typical perinuclear staining pattern. Confocal scanning laser microscopy revealed that the lamin A aggregates were indeed present throughout the internal nucleus. When these cells were extracted with Triton X-100 the nucleoplasmic aggregates disappeared, which indicates that the A-type lamins are not properly incorporated into the lamina. The A-type lamins in other cell lines derived from adenocarcinomas remained present in the nuclear periphery after extraction with the **non-ionic detergent**. Immunoblotting studies of the Triton X-100 soluble and insoluble fractions showed that lamin A and an apparently truncated product, which was detected with the lamin A antibody, were present in the insoluble fraction of GLC-A1. This truncated product is partly Triton X-100 soluble since it was also detected in the detergent soluble fraction. (ABSTRACT TRUNCATED AT 250 WORDS)

8/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08395768 95377528

A maternal **RNA** localized in the yellow crescent is segregated to the larval muscle cells during ascidian development.

Swalla BJ; Jeffery WR
Bodega Marine Laboratory, Bodega Bay, California 94923, USA.

Developmental biology (UNITED STATES) Aug **1995**, 170 (2) p353-64, ISSN 0012-1606 Journal Code: E7T
Contract/Grant No.: HD-07493, HD, NICHD; HD-13970, HD, NICHD
Languages: ENGLISH
Document type: JOURNAL ARTICLE

A cDNA library prepared from one-cell zygotes of the ascidian Styela clava was screened with probes from isolated cellular fractions to identify clones encoding RNAs localized in the yellow crescent or myoplasm, a cytoskeletal domain with multiple developmental roles. The differential screen yielded five overlapping cDNA (Styela clava yellow crescent or ScYC) clones encoding a 1.2-kb polyadenylated **RNA** (yellow crescent or YC **RNA**) which is present throughout embryonic development. In situ hybridization confirmed that YC **RNA** is localized in the yellow crescent. Antisense probes containing the 3' region of YC **RNA** hybridize with multiple maternal and zygotic RNAs, suggesting sequence homologies with other transcripts. YC **RNA** was first detected during oogenesis when transcripts accumulate in the perinuclear region of vitellogenic oocytes and are gradually translocated to the cortex. The YC transcripts are localized in the cortex of unfertilized eggs but after fertilization segregate with the myoplasm to the yellow crescent. During cleavage most YC transcripts enter the primary muscle cell lineage. YC **RNA** is also present in the secondary muscle cells. The YC transcripts are retained in the myoplasm of oocytes and eggs extracted with the **non-ionic detergent** Triton X-100, suggesting that they are associated with the cytoskeleton. The nucleotide sequence of the longest ScYC clone contains a short open reading frame (ORF). The YC ORF would encode a putative polypeptide of 49 amino acids, which shows no significant homology to known proteins. Several features of the YC **RNA**, however, suggest that it functions as an **RNA** rather than as a protein coding molecule. We conclude that the myoplasm contains a novel maternal **RNA** which is associated with the cytoskeleton and segregated to the muscle cells during ascidian embryogenesis. The YC **RNA** may be a new member of a growing family of noncoding RNAs that play important roles in growth and development.

8/3,AB/4 (Item 4 [redacted] file: 155)
DIALOG(R)File 155:MEDLINE(R)
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08210119 94356242
Hydrophilic and amphiphilic forms of Drosophila choline acetyltransferase are encoded by a single mRNA.
Salem N; Medilanski J; Pellegrinelli N; Eder-Colli L
Department of Pharmacology, Centre Medical Universitaire, Geneva, Switzerland.
European journal of neuroscience (ENGLAND) May 1 **1994**, 6 (5) p737-45, ISSN 0953-816X Journal Code: BYG
Languages: ENGLISH
Document type: JOURNAL ARTICLE
We have previously shown that the enzyme choline-O-acetyltransferase (ChAT) exists in a hydrophilic and an amphiphilic form in Drosophila head. A complementary DNA clone of 4.2 kb containing the entire coding region of ChAT was isolated from a cDNA library of Drosophila heads. The cDNA was subcloned in an expression vector and injected into the nucleus of Xenopus oocytes. Injected oocytes expressed high levels of ChAT activity. This activity was inhibited by bromoacetylcholine, a specific inhibitor of the enzyme. In the present study the **non-ionic detergent** Triton X-114 was used to analyse whether the expression of hydrophilic and amphiphilic ChAT was or was not directed by a single cDNA. The two forms of ChAT were found to be synthesized in injected oocytes. Approximately 9% of the recombinant enzyme partitioned as amphiphilic activity. This value was similar to that found for native amphiphilic ChAT in Drosophila heads. Sedimentation in sucrose gradients of amphiphilic enzyme was found to be influenced by the type of detergent present in the gradient whereas this was not the case for hydrophilic ChAT. Hydrophilic and amphiphilic enzyme activities differed in some of their biochemical properties. Amphiphilic ChAT was less sensitive to inhibition by the product acetylcholine than was hydrophilic ChAT. Moreover, amphiphilic ChAT was found to be more resistant than hydrophilic ChAT to heat inactivation at 45 degrees C. These properties were observed for the native as well as for recombinant ChAT. These results demonstrate that the hydrophilic and amphiphilic forms of ChAT are derived from one mRNA.

8/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

08054108 95058999
Translation and the cytoskeleton: a mechanism for targeted protein synthesis.
Hesketh J
Division of Biochemical Sciences, Rowett Research Institute, Bucksburn, Aberdeen, UK.
Molecular biology reports (NETHERLANDS) May **1994**, 19 (3) p233-43, ISSN 0301-4851 Journal Code: NGW
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL
This review describes the critical evidence that in eukaryotic cells polyribosomes, mRNAs and components of the protein synthetic machinery are associated with the cytoskeleton. The role of microtubules, intermediate filaments and microfilaments are discussed; at present most evidence suggests that polyribosomes interact with the actin filaments. The use of **non-ionic detergent** /deoxycholate treatment in the isolation of cytoskeletal-bound polysomes is described and the conclusion reached that at low salt concentrations this leads to mixed preparations of polysomes derived from both the cytoskeleton and the endoplasmic reticulum. At present the best approach for isolation of cytoskeletal-bound polysomes appears to involve extraction with salt concentrations greater than 130 mM

after an initial **non-ionic detergent** treatment. Such polysomes appear to be enriched in certain mRNAs and [redacted] it is suggested that they are involved in translation of a unique set of proteins. The evidence for mRNA localisation is presented and the role of the cytoskeleton in transport and localisation of **RNA** discussed. Recent data on the role of the 3' untranslated region in the targeting of mRNAs both to particular regions of the cell and for translation on cytoskeletal-bound polysomes is described. The hypothesis is developed that the association of polysomes with the cytoskeleton is the basis of a mechanism for the targeting of mRNAs and the compartmentalization of protein synthesis.

8/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07974916 94327726
Rapid and efficient purification of hepatitis A virus from cell culture.
Bishop NE; Hugo DL; Borovec SV; Anderson DA
Hepatitis Research Unit, Macfarlane Burnet Centre for Medical Research, Victoria, Australia.
Journal of virological methods (NETHERLANDS) Apr **1994**, 47 (1-2) p203-16, ISSN 0166-0934 Journal Code: HQR
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Hepatitis A virus (HAV) characteristically remains strongly cell-associated when grown in culture, with only small yields in the culture supernatant. Cell factories (6000 cm2) of BS-C-1 cells infected with the cytopathic HM175A.Z strain of HAV for 3, 4 or 7 days were harvested using trypsin to disperse the infected cell monolayer, and cells were collected by low speed centrifugation. More than 70% of the yield of virus and viral antigen can thus be obtained in the packed cell pellet. Packed cell pellets were resuspended in 5 volumes of isotonic buffer and cell membranes lysed by the addition of a **non-ionic detergent**. After removal of nuclei by centrifugation, ionic detergent was added to the clarified cytoplasmic extract. Under these conditions, HAV particles (virions and empty capsids) are the only particulate material remaining in the sample, and were recovered in a single ultracentrifugation step through discontinuous sucrose/glycerol density gradients. In one day, this method yields viral antigen with minimal cellular contaminants, in a concentrated volume suitable for subsequent biochemical, vaccine or diagnostic uses. The yield of viral antigen over numerous batches varied from 200 to 1600 vaccine-equivalent doses per cell factory, with a titre of up to 1 x 10(10) infectious particles per ml.

8/3,AB/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07879657 94155897
Purification, characterization and molecular cloning of human hepatic lysosomal acid lipase.
Ameis D; Merkel M; Eckerskorn C; Greten H
Department of Medicine, University Hospital Eppendorf, Hamburg, Germany.
European journal of biochemistry (GERMANY) Feb 1 **1994**, 219 (3) p905-14, ISSN 0014-2956 Journal Code: EMZ
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Lysosomal acid lipase (LAL) is a hydrolase essential for the intracellular degradation of cholesteryl esters and triacylglycerols. This report describes a multi-step procedure for the purification of LAL from human liver. After solubilization with **non-ionic detergent**, acid hydrolase activity was purified 17000-fold to

apparent homogeneity by sequential chromatography on Concanavalin A Sepharose, carboxymethyl cellulose, phenyl Superose, Mono S cation exchange and Superose 12 gel-filtration columns. This procedure yielded two silver-staining protein bands of 56 kDa and 41 kDa on SDS/PAGE. Size-exclusion chromatography of the 41-kDa protein indicated that the enzyme was catalytically competent as a monomer of approximately 38 kDa. When assayed in the presence of cholesteryl oleate or trioleoylglycerol, purified acid lipase had Vmax values of 4390 nmol fatty acid.min-1.mg protein and 4756 nmol fatty acid.min-1.mg protein-1, and apparent Km values of 0.142 mM and 0.138 mM, respectively. The purified enzyme was most active at low pH (4.5-5.0) and required **non-ionic detergent** and ethylene glycol for optimal stability. Incubation of the 41-kDa acid lipase with endoglucosaminidase H reduced the molecular mass by 4-6 kDa, demonstrating Asn-linked glycosylation with high-mannose oligosaccharides. Deglycosylation did not affect enzymic activity, indicating that carbohydrates are not required for LAL activity. Based on partial peptide sequence, an oligonucleotide was synthesized and utilized to isolate LAL cDNA clones from a human liver cDNA library. A full-length LAL cDNA contained 2626 nucleotides and coded for a predicted protein of 372 amino acids, preceded by a 27 residue hydrophobic signal peptide. Hepatic LAL differed from fibroblast acid lipase at the N-terminus and revealed extensive similarities with human gastric lipase and rat lingual lipase, confirming a gene family of acid lipases. Northern hybridization using the complete LAL cDNA as a radiolabeled probe indicated striking differences in mRNA expression among human tissues. LAL mRNA was most abundant in brain, lung, kidney and mammary gland. Placenta and HeLa cells expressed intermediate amounts of LAL mRNA, while **RNA** extracted from liver and heart showed low levels of expression.

8/3,AB/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07787567 94012987
Transport and localization of exogenous myelin basic protein mRNA microinjected into oligodendrocytes.
Ainger K; Avossa D; Morgan F; Hill SJ; Barry C; Barbarese E; Carson JH
Department of Biochemistry, University of Connecticut Health Center, Farmington 06030.
Journal of cell biology (UNITED STATES) Oct **1993**, 123 (2) p431-41, ISSN 0021-9525 Journal Code: HMV
Contract/Grant No.: NS15190, NS, NINDS; NS19943, NS, NINDS; RR03976, RR, NCRR
Languages: ENGLISH
Document type: JOURNAL ARTICLE
We have studied transport and localization of MBP mRNA in oligodendrocytes in culture by microinjecting labeled mRNA into living cells and analyzing the intracellular distribution of the injected **RNA** by confocal microscopy. Injected mRNA initially appears dispersed in the perikaryon. Within minutes, the **RNA** forms granules which, in the case of MBP mRNA, are transported down the processes to the periphery of the cell where the distribution again becomes dispersed. In situ hybridization shows that endogenous MBP mRNA in oligodendrocytes also appears as granules in the perikaryon and processes and dispersed in the peripheral membranes. The granules are not released by extraction with **non-ionic detergent**, indicating that they are associated with the cytoskeletal matrix. Three dimensional visualization indicates that MBP mRNA granules are often aligned in tracks along microtubules traversing the cytoplasm and processes. Several distinct patterns of granule movement are observed. Granules in the processes undergo sustained directional movement with a velocity of approximately 0.2 micron/s. Granules at branch points undergo oscillatory motion with a mean displacement of 0.1 micron/s. Granules in the periphery of the cell circulate randomly with a mean displacement of approximately 1 micron/s.

The results are discussed in terms of a multi step pathway for transport and localization of MBP mRNA in oligodendrocytes. This work represents the first characterization of intracellular movement of mRNA in living cells, and the first description of the role of **RNA** granules in transport and localization of mRNA in cells.

8/3,AB/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07735221 94171936
Generation of truncated brain AE3 isoforms by alternate mRNA processing.
Morgans CW; Kopito RR
Department of Biological Sciences, Stanford University, CA 94305-5020.
Journal of cell science (ENGLAND) Dec **1993**, 106 (Pt 4) p1275-82
, ISSN 0021-9533 Journal Code: HNK
Languages: ENGLISH
Document type: JOURNAL ARTICLE
AE3 gene is a member of the AE anion exchanger gene family that is expressed primarily in brain and heart. The principal product of the AE3 gene in rodent brain, FL-AE3p, when expressed in heterologous cell lines, gives rise to chloride-dependent changes in intracellular pH consistent with its operation as an anion exchanger. We have identified two novel isoforms of mouse AE3 that are generated by tissue-specific alternate **RNA** processing. One of these isoforms encodes a polypeptide, 14-AE3p, that corresponds to a portion of the NH2-terminal cytoplasmic domain of AE3. 14-AE3p lacks the entire transmembrane domain that-in FL-AE3p forms the anion exchange channel. Immunoblots with antibodies to the NH2- and COOH-termini confirm that FL-AE3 and 14-AE3 are expressed in rat brain as 160 kDa and 74 kDa polypeptides, respectively. Unlike FL-AE3p, however, 14-AE3p is insoluble in **non-ionic detergent**, suggesting a possible association with the cytoskeleton.

8/3,AB/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07472829 92339451
Prosomes and their multicatalytic proteinase activity.
Nothwang HG; Coux O; Bey F; Scherrer K
Institut Jacques Monod, CNRS, Universite Paris 7, France.
European journal of biochemistry (GERMANY) Jul 15 **1992**, 207 (2) p621-30, ISSN 0014-2956 Journal Code: EMZ
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Prosomes were first described as being mRNA-associated RNP (ribonucleoprotein) particles and subcomponents of repressed mRNPs (messenger ribonucleoprotein). We show here that prosomes isolated from translationally inactive mRNP have a protease activity identical to that described by others for the multicatalytic proteinase complex (MCP, 'proteasome'). By RNase or **non-ionic detergent** treatment, the MCP activity associated with repressed non-globin mRNP from avian erythroblasts, sedimenting at 35 S, could be quantitatively shifted on sucrose gradients to the 19-S sedimentation zone characteristic of prosomes, which were identified by monoclonal antibodies. The presence of small **RNA** in the enzymatic complex was shown by immunoprecipitation of the protease activity out of dissociated mRNP using a mixture of anti-prosome monoclonal antibodies; a set of small RNAs 80-120 nucleotides long was isolated from the immunoprecipitate. Furthermore, on CsCl gradients, colocalisation of the MCP activity with prosomal proteins and prosomal **RNA** was found, and no difference in the prosomal **RNA** pattern was observed whether the particles were fixed or not prior to centrifugation. These data indicate that the MCP activity is a property of

prosomes, shown to be in part RNP and subcomplexes of in vivo uninitiated mRNP. A hypothesis for the role of the prosome-MCP particles in maintaining homeostasis of specific protein levels is proposed.

8/3,AB/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07129231 93008478
In vitro activation of heat shock transcription factor by 4-hydroxynonenal.
Cajone F; Crescente M
Istituto di Patologia Generale, 'Universita degli Studi di Milano, Italy.
Chemico-biological interactions (NETHERLANDS) Sep 28 **1992**, 84 (2) p97-112, ISSN 0009-2797 Journal Code: CYV
Languages: ENGLISH
Document type: JOURNAL ARTICLE
In the activation of eukaryotic heat shock genes, the acquisition of a binding ability to specific DNA sequence by a transcriptional activator, heat shock factor (HSF), is believed to be a crucial step. The induction of this new DNA binding activity of HSF is also obtained in a cell-free system (in vitro activation) by hyperthermia or at physiological temperature by calcium ions, low pH, urea, or **non-ionic detergent**. We report here the in vitro activation of HSF by treating at 0 degrees C a HeLa cell-free system with the aldehyde 4-hydroxynonenal (HNE), a highly cytotoxic product of lipid peroxidation. The in vitro activation of HSF by HNE occurred only if some components of the cell-free system were not sedimented at 100,000 x g. The reason for this is unclear but the release of active HSF from nuclei of unshocked cells and the involvement of Ca2+ contained in the mitochondria and ER have been excluded. Although HNE is known to be a sulfhydryl blocking agent, the results obtained with N-ethylmaleimide suggest that different mechanisms might be involved in the in vitro activation of HSF by HNE.

8/3,AB/12 (Item 12 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06823184 92070562
Cleavage reaction of a synthetic oligoribonucleotide corresponding to the autocleavage site of a precursor **RNA** from bacteriophage T4.
Hosaka H; Ogawa T; Sakamoto K; Yokoyama S; Takaku H
Department of Industrial Chemistry, Chiba Institute of Technology, Japan.
FEBS letters (NETHERLANDS) Nov 18 **1991**, 293 (1-2) p204-6, ISSN 0014-5793 Journal Code: EUH
Languages: ENGLISH
Document type: JOURNAL ARTICLE
A fragment (GUUUCGUACAAAC) having a consensus sequence for the self-cleavage domain in a precursor of an **RNA** molecule from T4-infected Escherichia coli cells (p2Sp1; precursor of species 1) was chemically synthesized and found to be cleaved either between CA (139-140) or between UA (137-138) in the presence of monovalent cations and a **non-ionic detergent**. The cleaved products had 5'-hydroxyl and 3'-phosphate groups, of which some were in the form 2',3'-cyclic phosphates.

8/3,AB/13 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06578819 91346637
The double-stranded **RNA** associated with the '447' cytoplasmic male

sterility in Vicia faba is packaged together with its replicase in cytoplasmic membranous vesicles.

Lefebvre A; Scalla R; Pfeiffer P

Station d'Amelioration des Plantes, Institut National de la Recherche Agronomique, Dijon, France.

Plant molecular biology (NETHERLANDS) Apr **1990**, 14 (4) p477-90, ISSN 0167-4412 Journal Code: A60

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The 447 male sterility trait in Vicia faba is strictly correlated with the presence of well-defined membranous vesicles or 'cytoplasmic spherical bodies' not found in fertile isogenic maintainer plants, and by the occurrence of a discrete high molecular weight double-stranded **RNA**. We have purified these cytoplasmic membranous vesicles and find that they contain the dsRNA together with an **RNA**-dependent **RNA** polymerase whose activity depends upon the presence of Mg2+, requires the four-nucleoside triphosphates and is unaffected by inhibitors of cellular transcriptases, e.g. alpha-amanitin and Actinomycin D. The dsRNA can be labelled in vitro by incubating the cytoplasmic vesicles with radioactive NTPs, and the **RNA** synthesized in vitro is also in a double-stranded form as judged by its resistance to RNase digestion at high salt and its behaviour upon CF-11 chromatography. Treatment of the vesicles with a **non-ionic detergent** releases the dsRNA in the form of a complex with the **RNA**-dependent **RNA** polymerase. The enzyme can still carry out the specific synthesis of dsRNA in these solubilized complexes. The cytoplasmic vesicles therefore isolate this vertically transmitted, self-replicating dsRNA from the cellular milieu: the possible mode of action and relevance of this novel genetic element to the 447 cytoplasmic male sterility trait are discussed.

8/3,AB/14 (Item 14 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

06298001 86182143

A disappearance of a 24-kDa acid-soluble protein from liver chromatin of normal and starved hens following D-galactosamine administration.

Palyga J

Zeitschrift fur Naturforschung. Section C: Biosciences (GERMANY, WEST) Nov-Dec **1985**, 40 (11-12) p798-805, ISSN 0341-0382 Journal Code: XYX

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Normal and starved adult chickens were injected intraperitoneally with D-galactosamine hydrochloride (0.5 g/kg body weight) and 6 h later liver chromatin acid-soluble proteins were isolated. These proteins were resolved by a two-dimensional polyacrylamide gel electrophoresis in the presence of **non-ionic detergent**, Triton X-100, in the first dimension and anionic detergent, sodium dodecyl sulfate, in the second dimension. Although spotting patterns of acid-soluble chromatin proteins were remarkably similar between normal and starved control birds and those receiving D-galactosamine, a disappearance of a 24-kDa protein after administration of this agent was found. Moreover, it was shown that this protein was also completely absent in the chicken erythrocyte chromatin which was known to be inactive in **RNA** synthesis. It seems that the disappearance of the 24-kDa chromatin protein may be associated with inhibiting of transcription in hen liver after D-galactosamine administration and during hen erythrocyte maturation.

8/3,AB/15 (Item 15 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

06119302 86072619

Human parainfluenz[redacted]virus 3: purification and [redacted]racterization of subviral components, viral proteins and viral **RNA**.

Wechsler SL; Lambert DM; Galinski MS; Heineke BE; Pons MW

Virus research (NETHERLANDS) Nov **1985**, 3 (4) p339-51, ISSN 0168-1702 Journal Code: X98

Languages: ENGLISH

Document type: JOURNAL ARTICLE

A simple method was established that allowed large quantities of human parainfluenza 3 (PF3) virions to be isolated from tissue culture cells. The purity of the virus was sufficient for biochemical analysis of virion proteins. The density of PF3 virions was 1.18-1.20. Purified virions contained seven viral proteins with estimated molecular weights of: L, 180 000; P, 83 000; HN, 69 000; NP, 66 000; F0, 60 000; F1, 51 000; and M, 38 000, as determined by sodium dodecyl sulfate-polyacrylamide gel electrophoresis under reducing conditions. There were three phosphoproteins, P, NP and M, and two glycoproteins, HN and F (includes F0 and F1). F1.2, the activated, cleaved, fusion glycoprotein (60 000 Da), consisting of two disulfide-linked subunits, F1 and F2, was seen only under nonreducing conditions. Because of its small size (approximately 9000 Da) F2 could be seen only on gels with high acrylamide concentrations. As in other enveloped viruses, cellular actin (43 000 Da) was present in purified virions. Several minor bands migrating between NP and M represented breakdown products of NP. Solubilization of the virion membrane in low salt buffer with **non-ionic detergent** resulted in the loss of HN and F. In high salt buffer, the M protein was also removed. Nucleocapsids isolated by CsCl centrifugation contained L, P, NP and small amounts of M. Nucleocapsids isolated in the presence of the ionic detergent, sarcosyl, contained only the NP protein. The density of nucleocapsids was 1.29-1.30. Genomic 50S **RNA** isolated from nucleocapsids had an estimated molecular weight of 5 X 10(6).

8/3,AB/16 (Item 16 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

05828751 88093176

Particles with properties of retroviruses in monocytes from patients with breast cancer [see comments]

Al-Sumidaie AM; Leinster SJ; Hart CA; Green CD; McCarthy K

University Department of Surgery, University of Liverpool.

Lancet (ENGLAND) Jan 2-9 **1988**, 1 (8575-6) p5-9, ISSN 0140-6736 Journal Code: L0S

Comment in Lancet 1990 Oct 27;336(8722):1079

Languages: ENGLISH

Document type: JOURNAL ARTICLE

An agent with the properties of a retrovirus has been detected regularly in monocytes from patients with breast cancer. In 97% of breast cancer patients the cell-free culture medium (CFCM) in which the monocytes had been cultured possessed reverse transcriptase (RT) activity. In contrast, RT activity was detected in the CFCM from only 11% of age and sex matched controls (p less than 0.0001; Wilcoxon rank sum test). The RT activity was associated with particles having a buoyant density of between 1.165 and 1.18 g/ml, similar to that of retroviruses. Treatment of the samples with **non-ionic detergent** abolished the peaking of the activity in this fraction. Enveloped particles (100-120 nm in diameter) with a fringed surface resembling murine mammary tumour virus were found on negative-stain electron microscopy in CFCM obtained from patients with breast cancer. Retrovirus-like particles were also observed in the cytoplasm of giant cells formed by monocytes from these patients, and also in macrophages in breast cancer tissue; however, no such particles were detected in the tumour cells. These findings strongly suggest the presence of a retrovirus in the monocytes from patients with breast cancer. The importance of these observations in the pathophysiology of carcinoma of the

8/3,AB/17 (Item 17 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05803411 86109176
Studies of developmental abnormalities at the molecular level of mouse embryos homozygous for the t12 lethal mutation.
Nozaki M; Iwakura Y; Matsushiro A
Developmental biology (UNITED STATES) Jan **1986**, 113 (1) p17-28, ISSN 0012-1606 Journal Code: E7T
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Embryos obtained by crossing heterozygous t12 mutant mice were labeled metabolically with 14C-amino acids at the mid-morula stage, and the protein pattern of single embryos was examined by two-dimensional polyacrylamide gel electrophoresis. After labeling, the morphology was still normal. The genotypes of the embryos could be identified by the allelic forms of Tcp-1 (p63/6.9) protein on the gel. In t12/t12 embryos, the bulk of syntheses of macromolecules such as proteins and RNAs [poly(A)+, as well as poly(A)- **RNA**] was normal, however, syntheses of several proteins were markedly reduced. Some of these proteins present in reduced amounts appeared to be components of cytokeratin-type intermediate filaments (endo A and endo B), judging from their insolubility in **non-ionic detergent**, their appearance in the mid-morula stage, their location in trophectodermal cells, and their electrophoretic mobilities. These observations suggest that mechanisms for the induction of the intermediate filament proteins are defective in embryos homozygous for the t12 mutation. Possible relationships between the morphological abnormalities of the embryos and their defective synthesis of intermediate filaments are discussed.

8/3,AB/18 (Item 18 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05214946 86056072
Nuclear substructure antigens. Monoclonal antibodies against components of nuclear matrix preparations.
Lehner CF; Eppenberger HM; Fakan S; Nigg EA
Experimental cell research (UNITED STATES) Jan **1986**, 162 (1) p205-19, ISSN 0014-4827 Journal Code: EPB
Languages: ENGLISH
Document type: JOURNAL ARTICLE
We describe two monoclonal antibodies, I-2 and I-14, which recognize, respectively, proteins of 36 and 40 kD. By immunofluorescence microscopy on chick embryo fibroblasts, both antigens were found to be located within a nuclear substructure which excludes nucleoli and part of the nucleoplasm; hence we refer to these antigens as nuclear substructure antigens. By immuno-electron microscopy on chick liver sections, the I-14 antigen was identified predominantly in clusters of interchromatin granules and in perichromatin fibrils. The two substructure antigens share a remarkable resistance to sequential extraction of nuclei with DNase I, RNase A, **non-ionic detergent** and high salt, indicating that they constitute part of an operationally defined residual nuclear matrix. Finally, both substructure antigens are virtually absent from the nuclei of adult erythrocytes. These properties suggest that substructure antigens may be involved in **RNA** transcription, processing or transport, possibly by contributing nucleoskeletal support.

8/3,AB/19 (Item 19 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05209510 89034472
Tobacco mosaic virus replicase and replicative structures.
Young N; Forney J; Zaitlin M
Department of Plant Pathology, Cornell University, Ithaca, New York 14853.
Journal of cell science. Supplement (ENGLAND) **1987**, 7 p277-85, ISSN 0269-3518 Journal Code: HNG
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The **RNA**-dependent **RNA** polymerase (replicase) mediating the replication of tobacco mosaic virus (TMV) has been investigated in a number of laboratories over a period of 20 years. Cell-free enzyme preparations have been prepared which can continue the synthesis of nascent complementary **RNA**, initiated in vivo; however, the enzyme does not require, nor does it respond to, exogenous viral **RNA** as a template. The presence in plants of a virus-stimulated, host-encoded **RNA**-dependent **RNA** polymerase (RdRp) has added confusion to this field; it is now generally conceded, however, that this enzyme is not the TMV replicase. Our recent studies have emphasized several aspects of TMV **RNA** replication. We have examined the nature of TMV replicative structures synthesized in vitro by utilizing a partially purified enzyme preparation isolated from TMV-infected tobacco tissue. Radiolabelled products of the reaction were analysed on agarose gels and fractions with the predicted electrophoretic migration and nuclease sensitivities of replicative form (RF) and replicative intermediate (RI) were isolated. These fractions were hybridized to a collection of bacteriophage M13 clones containing portions of the TMV genome of both plus and minus polarity. The nascent synthesis in the RI-like molecules was restricted to the plus viral strand, while the new synthesis in the RF-like molecules was of both plus and minus polarity. Solubilization of the membrane-bound replicase with the **non-ionic detergent** CHAPS has yielded complexes which remain in solution after high-speed centrifugation. The solubilized replication complexes have been utilized as starting material for enzyme purification by Sepharose 4B gel filtration chromatography. The intracellular site of synthesis of TMV **RNA** has been reinvestigated in the light of reports suggesting a nuclear site of replication. The conclusion for nuclear synthesis has been based on fractionation of subcellular homogenates of virus-infected leaves or mesophyll protoplasts and identification of virus-related proteins associated with these fractions. In our studies, however, we conclude that these procedures can be misleading in that the 126,000 Mr TMV protein (and replicase activity) were found in all fractions of the homogenate analysed. Double-stranded TMV **RNA**, on the other hand, was barely detectable in preparations of purified nuclei; instead it was concentrated in the post-nuclear supernatant, suggesting that the nucleus is not the site of TMV **RNA** synthesis.

8/3,AB/20 (Item 20 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05121681 88054980
A cell-free plant extract for accurate pre-tRNA processing, splicing and modification.
Stange N; Beier H
Institut fur Biochemie, Bayerische Julius-Maximilians-Universitat, Wurzburg, FRG.
EMBO journal (ENGLAND) Sep **1987**, 6 (9) p2811-8, ISSN 0261-4189 Journal Code: EMB
Languages: ENGLISH
Document type: JOURNAL ARTICLE
An intron-containing tobacco tRNA(Tyr) precursor synthesized in a HeLa

cell nuclear extract has been used to develop a cell-free processing and splicing system from wheat germ. Removal of 5' and 3' flanking sequences, accurate excision of the intervening sequence, ligation of the resulting tRNA halves, addition of the 3'-terminal CCA sequence and modification of seven nucleosides were achieved in appropriate wheat germ S23 and S100 extracts. The maturation of pre-tRNA(Tyr) in these extracts resembles the pathway observed in vivo for tRNA biosynthesis in Xenopus oocytes and yeast in that processing of the flanks precedes intron excision. Most of the modified nucleosides (m2(2) G, psi 35, psi 55, m7G and m1A) are introduced into the intron-containing pre-tRNA with mature ends, whereas two others (m1G and psi 39) are only found in the mature tRNA(Tyr). Processing and splicing proceed very efficiently in the wheat germ extracts, leading to complete maturation of 5' and 3' ends followed by about 65% conversion to mature tRNA(Tyr) under our standard conditions. The activity of the wheat germ endonuclease is stimulated 3-fold by the **non-ionic detergent** Triton X-100. All previous attempts to demonstrate the presence of a splicing endonuclease in wheat germ had failed (Gegenheimer et al., 1983). Hence, this is the first cell-free plant extract which supports pre-tRNA processing and splicing in vitro.

8/3,AB/21 (Item 21 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04970089 87054303
Cytoskeletal association of muscle-specific mRNAs in differentiating L6 rat myoblasts.
Bagchi T; Larson DE; Sells BH
Experimental cell research (UNITED STATES) Jan **1987**, 168 (1) p160-72, ISSN 0014-4827 Journal Code: EPB
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The importance of the cytoskeleton in protein synthesis was studied in differentiating L6 rat myoblasts. Soluble and cytoskeletal fractions obtained after gentle, **non-ionic detergent** lysis of myoblasts and myotubes were analysed for the presence of ribosomes and mRNPs. Polysomal mRNPs were predominantly associated with the cytoskeletal framework and free mRNPs were present in both soluble and cytoskeletal fractions. An examination of the distribution of specific mRNAs in the polysomal and free mRNP populations of both cytoplasmic fractions revealed differences in the pattern of their distribution. It is further demonstrated that in the L6 rat myoblast system, ribosomes and mRNA (or mRNP) are not associated with the microfilaments, unlike in other systems studied.

8/3,AB/22 (Item 22 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04591463 85140060
Low-speed purification of human placental nuclei.
Resendez-Perez D; Barrera-Saldana HA; Morales-Vallarta MR; Ramirez-Bon E; Leal-Garza CH; Feria-Velazco A; Sanchez-Anzaldo FJ
Placenta (ENGLAND) Nov-Dec **1984**, 5 (6) p523-32, ISSN 0143-4004 Journal Code: PMN
Languages: ENGLISH
Document type: JOURNAL ARTICLE
A simple method for the purification of human placental nuclei is described. Nuclei were isolated by homogenizing tissue in standard saline citrate solution in the presence of zinc chloride to stabilize the nuclear membranes, NP40 as **non-ionic detergent** and sodium bisulphite for inhibition of proteolytic activity. Nuclei purification was achieved by low-speed centrifugation through a discontinuous sucrose

gradient. The purified nuclei were evaluated by morphological criteria using phase contrast and electron microscopy. The extent of contamination by cytoplasmic debris was estimated by Papanicolaou's staining technique. Biochemical criteria include measurements of alkaline phosphatase activity as a plasma membrane enzyme marker and DNA-dependent **RNA** polymerase activity for the functional integrity of nuclear components. Transcriptionally active nuclei were obtained but the yield of nuclei was low; however, this low yield is compensated by the high degree of purity, the simplicity of the method and the functional and morphological integrity of the purified nuclei.

8/3,AB/23 (Item 23 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04564455 83221341
Purification and characterization of the **RNA** polymerases of the sea urchin, Lytechinus variegatus.
Sittman DB; Stafford DW
Preparative biochemistry (UNITED STATES) **1983**, 13 (1) p21-39, ISSN 0032-7484 Journal Code: PL5
Languages: ENGLISH
Document type: JOURNAL ARTICLE
We have identified four forms of sea urchin **RNA** polymerase (Ia, Ib, II and III). Three of the forms co-elute on DEAE cellulose chromatography but separate on DEAE Sephadex chromatography. The separation of these three enzyme forms by DEAE Sephadex chromatography can be eliminated with **non-ionic detergent**. We also demonstrate that either form I or form III **RNA** polymerase loses its resistance to alpha-amanitin after DEAE chromatography. A procedure for the purification of combined form I and III **RNA** polymerase and the purification of **RNA** polymerase II is also presented.

8/3,AB/24 (Item 24 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04542773 82098297
Conformational changes induced by salt in complexes of histones and superhelical nuclear DNA.
Levin JM; Cook PR
Journal of cell science (ENGLAND) Aug **1981**, 50 p199-208, ISSN 0021-9533 Journal Code: HNK
Languages: ENGLISH
Document type: JOURNAL ARTICLE
When HeLa cells are lysed in solutions containing a **non-ionic detergent** and 0.75 M-NaCl, structures are released that retain many of the morphological features of nuclei. These nucleoids contain all the nuclear DNA, **RNA** and the 'core' histones, but few other proteins characteristic of chromatin. Their DNA is intact. The core histones dissociate on raising the salt concentration. We have probed the structure of nucleoid-histone complexes using the intercalating dye, ethidium, or the **RNA** polymerase of Escherichia coli. Both have a higher affinity for superhelical DNA than they do for relaxed DNA. The binding of ethidium is measured fluorometrically, and using this probe we find that the DNA of nucleoids containing all the core histones behaves as if it were supercoiled slightly positively. As the salt concentration is increased, free energy characteristic of negative supercoiling appears between 0.92 M and 0.95 M-NaCl. This transition, which is reversible in the presence of the arginine-rich histones, occurs without dissociation of these histones from the DNA and so must reflect a conformational change in the complex. In contrast to the results with ethidium, we find that **RNA** polymerase can detect the presence of some negative free energy of supercoiling in

nucleoids containing the core histones. The transformations of the free energy that can assist the binding of ethidium and **RNA** polymerase are discussed.

8/3,AB/25 (Item 25 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04496749 82167298
Reverse transcriptase associated with avian sarcoma-leukosis viruses. I. Comparison of intra-virion content of multiple enzyme forms.
Ueno A; Ishihama A; Toyoshima K
Journal of biochemistry (JAPAN) Jan **1982**, 91 (1) p311-22, ISSN 0021-924X Journal Code: HIF
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The **RNA**-dependent DNA polymerase (the reverse transcriptase) was solubilized from three related strains of avian sarcoma virus (ASV B77, ASV tsLA334, and ASV QV2) as well as avian myeloblastosis virus (AMV) and a chicken endogenous virus (RAV-0), by a combination of **non-ionic detergent** treatment and CsCl step-gradient centrifugation, and was subsequently separated into individual enzyme forms by poly(C)-agarose column chromatography. The newly developed two-step method allowed us to purify the three molecular forms (alpha-, alpha beta- and beta-form) of highly active enzyme rapidly and quantitatively from all the five virus strains examined. The molar ratio of the three enzyme forms differed among the virus strains: For the three sarcoma viruses, the major species was the alpha beta-form enzyme, the putative holoenzyme, and the alpha- and beta-form enzymes were less than a few percent and 15-25%, respectively, while the alpha-form enzyme content was higher for the two leukosis viruses than for the three sarcoma viruses. Both the total DNA polymerase activity and the content of the two enzyme subunits in purified virions of the three sarcoma virus was in the following order: ASV tsLA334 greater than ASV B77 greater than ASV QV2, which paralleled the virus yield at a permissive temperature in roller bottle cultures of chick embryo fibroblasts. No alteration was found in the thermolability of DNA polymerases between tsLA334, which carries ts mutations affecting both virus growth and cell-transformation, and other viruses.

8/3,AB/26 (Item 26 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04483992 85157843
Replication and transcription depend on attachment of DNA to the nuclear cage.
Jackson DA; McCready SJ; Cook PR
Journal of cell science. Supplement (ENGLAND) **1984**, 1 p59-79, Journal Code: HNG
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW
When living cells are lysed in a **non-ionic detergent** and 2 M-NaCl, structures are released that resemble nuclei. They contain naked nuclear DNA packaged within a flexible cage of **RNA** and protein. Since the DNA is supercoiled, it must be intact and looped by attachment to the cage. It is argued that this cage is the active site of the key nuclear functions, transcription and replication: outlying sequences are activated by attachment to polymerases at the cage. This thesis is supported by the close and specific association of nascent **RNA** with cages, the attachment of active viral sequences (in transformed and productively infected cells) and the attachment of nascent DNA during both normal and repair synthesis.

8/3,AB/27 (Item 27 [redacted]om file: 155)
DIALOG(R)File 155:MEDLINE(R)
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04476524 84231330
Characterization of the **RNA** dependent DNA polymerase of a new human T-lymphotropic retrovirus (lymphadenopathy associated virus).
Rey MA; Spire B; Dormont D; Barre-Sinoussi F; Montagnier L; Chermann JC
Biochemical and biophysical research communications (UNITED STATES) May 31 **1984**, 121 (1) p126-33, ISSN 0006-291X Journal Code: 9Y8
Languages: ENGLISH
Document type: JOURNAL ARTICLE
We described here the characteristics of the Reverse Transcriptase activity associated with the Lymphadenopathy Associated Virus (LAV). A critical concentration of **non ionic detergent**, all four deoxyribonucleosides triphosphates and the divalent cation Mg2+ are required for optimal endogenous enzyme activity. The endogenous reaction product is digested by DNase and not by RNase and its synthesis is only slightly inhibited by actinomycin D. Exogenous reactions are optimal using poly A oligo dT12 -18 or poly Cm oligo dG12 -18 as template primer and Mg2+ as divalent cation. This enzyme can be distinguished from other cellular DNA polymerases activities and from Terminal deoxynucleotidyl Transferase (TdT) by purification from LAV infected T lymphocytes using phosphocellulose column.

8/3,AB/28 (Item 28 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

04450090 82113332
Effect of treatment with Triton X-100 on DNA integrity and DNA:**RNA**: protein ratio of rat liver nuclei]
Effetto del trattamento con Triton X-100 sull'integrita del DNA e sul rapporto DNA:**RNA**:proteine di nuclei di fegato di ratto.
Carlo P; Martelli A; Bignone FA
Bollettino della Societa italiana di biologia sperimentale (ITALY) Nov 30 **1981**, 57 (22) p2203-8, ISSN 0037-8771 Journal Code: ALS
Languages: ITALIAN Summary Languages: ENGLISH
Document type: JOURNAL ARTICLE ; English Abstract
A procedure is described that gives clean nuclei with intact DNA from a rat liver cell suspension. Cytoplasmic contamination is removed by successive treatments with a **non ionic detergent**, Triton X-100 (0.75%, v/v). We found that with ratios DNA:**RNA**: protein of 1:0.09:3.29 (2 Triton X-100 steps) the integrity of DNA is preserved: further decrease in **RNA** and protein content (3 Triton X-100 steps) causes DNA breakage, probably because of extraction of nuclear proteins. In order to estimate DNA integrity, its viscosity was determined by the use of a new oscillating crucible viscometer; this method makes possible the evaluation of extremely small levels of DNA damage as that induced by 0.067 mg/kg of DMNA injected i.p.

8/3,AB/29 (Item 29 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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04051814 85003597
A general method for preparing intact nuclear DNA.
Cook PR
EMBO journal (ENGLAND) Aug **1984**, 3 (8) p1837-42, ISSN 0261-4189 Journal Code: EMB
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Naked nuclear DNA [redacted] easily sheared. Two general methods are described for preparing intact [redacted]NA in a stable form that can [redacted] pipetted without breaking it. Cells are encapsulated in agarose microbeads and then lysed in a **non-ionic detergent** (i.e., Triton X-100) and 2 M NaCl or an ionic detergent (e.g., sodium or lithium dodecyl sulphate) in low salt. Most cellular protein and **RNA** then diffuse out through pores in the beads to leave encapsulated and naked DNA which is nevertheless accessible to enzymes and other probes. Remarkably, considerable structure is preserved since the DNA is supercoiled and chromosomes retain their shape.

8/3,AB/30 (Item 30 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03777754 82098298
Reconstruction of complexes of histone and superhelical nuclear DNA.
Levin JM; Cook PR
Journal of cell science (ENGLAND) Aug **1981**, 50 p209-24, ISSN 0021-9533 Journal Code: HNK
Languages: ENGLISH
Document type: JOURNAL ARTICLE
When HeLa cells are lysed in solutions containing a **non-ionic detergent** and 2 M-NaCl, structures are released that retain many of the morphological features of nuclei. These nucleoids contain all the nuclear **RNA** and DNA but few of the proteins characteristic of chromatin. Their DNA is supercoiled and so intact. Using a simple and rapid procedure we have reconstructed nucleohistone complexes from nucleoids and the 'core' histones without breaking the DNA. We have probed the integrity and structure of the reconstructed complexes using a non-destructive fluorometric approach, which provides a general method for detecting agents that bind to DNA and alter its supercoiling. The superhelical status of the DNA in the reconstructed complexes is indistinguishable from that found in control nucleoids containing core histones. Experiments with micrococcal nuclease confirm that the DNA in the reconstructed complexes is organized into nucleosome-like structures. These, however, are spaced 145 base-pairs apart and not 200 base-pairs apart as is found in native chromatin.

8/3,AB/31 (Item 31 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03463390 82032291
Comparisons of Belmont virus, a possible bunyavirus unique to Australia, with bunyamwera virus.
McPhee DA; Westaway EG
Journal of general virology (ENGLAND) May **1981**, 54 (Pt 1) p135-47, ISSN 0022-1317 Journal Code: I9B
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Belmont virus is an arbovirus isolated from mosquitoes and has a preference for marsupial hosts. The diameter of virions by negative staining (122 nm before fixation and 91 nm after fixation) was greater than that of Bunyamwera virus (94 nm and 79 nm respectively). However, the particles of both viruses appeared morphologically identical and sedimented at the same rate in sucrose density gradients. Belmont virus had a tripartite segmented **RNA** genome (28S, 24S and 11S) similar to Bunyamwera virus **RNA** (33S, 26S and 16S). The mol. wt. of these **RNA** species of Belmont virus measured by gel electrophoresis was 3.2 x 10(6), 2.4 x 10(6) and 0.3 x 10(6) compared to 2.9 x 10(6), 1.8 x 10(6) and 0.3 x 10(6) for the L, M and S species of Bunyamwera virus **RNA**. Both viruses comprised four structural proteins of the same relative proportions and corresponding mol. wt. For Bunyamwera virus, these were 145

x 10(3) (L), 104 x 10(3) (G1), 32 x 10(3) (G2) and 22 x 10(3) (N). The equivalent proteins of Belmont virus had mol. wt. of 147 x 10(3) (P147), 107 x 10(3) (G107), 28 x 10(3) (P28) and 25 x 10(3) (P25). Under conditions in which the envelope glycoproteins G1 and G2 of Bunyamwera virus were labelled in glucosamine, only G107 of Belmont virus was labelled. However, both G107 and P28 of Belmont virus were solubilized by **non-ionic detergent** and were then separable from the nucleocapsid containing all the **RNA** and P25. Chymotrypsin treatment of Belmont virus digested only G107, leaving a residue of P25 and P28, and of visible spikes. Similarly, G2 and the spikes of Bunyamwera virus resisted digestion with chymotrypsin. It was concluded that P28 is an envelope protein, equivalent to G2. Belmont virus thus appears to be a typical member of the Bunyaviridae but is unique in that it lacks carbohydrate in the small envelope protein (P28).

8/3,AB/32 (Item 32 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03452301 82007994
Repair of strand breaks in superhelical DNA of ataxia telangiectasia lymphoblastoid cells.
Lavin MF; Davidson M
Journal of cell science (ENGLAND) Apr **1981**, 48 p383-91, ISSN 0021-9533 Journal Code: HNK
Languages: ENGLISH
Document type: JOURNAL ARTICLE
A number of different assay methods have been used to study repair of strand breaks in DNA after exposure of cells to ionizing radiation. Use of these methods indicates that fibroblasts from patients with ataxia telangiectasia (AT), a multiform genetic disease exhibiting high sensitivity to ionizing radiation, have a normal ability to repair strand breaks in DNA. All of these methods determine the extent of breakage of DNA and the resealing of these breaks but do not provide information on restoration of DNA configuration in the nucleus. In this report we have used a sensitive technique to investigate restoration of the 3-dimensional structure of DNA in AT lymphoblastoid cells after exposure to ionizing radiation. This technique provides a means of lysing cells using a high concentration of salt and a **non-ionic detergent**, giving rise to structures called nucleoids which contain nuclear **RNA** and DNA, are depleted in protein, and sediment in a manner characteristic of supercoiled DNA. We have shown that the degree of supercoiling is the same in control and AT lymphoblastoid cells using sedimentation in the presence of ethidium bromide. The extent of breakage after exposure of cells to gamma-radiation, and the rate of repair of these breaks are similar in both cell types. Rate of repair of strand breaks is dose dependent and the restructured rapidly sedimenting complex behaves similarly, on sucrose gradients containing ethidium bromide, to that extracted from unirradiated cells.

8/3,AB/33 (Item 33 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03189363 78067048
Mass isolation ofpolytene nuclei from Chironomus salivary glands.
Mahr R; Lezzi M; Eppenberger HM
Journal of cell science (ENGLAND) **1977**, 27 p1-12, ISSN 0021-9533 Journal Code: HNK
Languages: ENGLISH
Document type: JOURNAL ARTICLE
In this paper we describe a method for the rapid mass isolation of polytene nuclei from Chironomus salivary glands. The procedure for the

isolation of glands involves 5 principal steps; (a) freezing Chironomus larvae in liquid prop[redacted] (b) breaking open frozen ani[redacted]s in a pre-cooled mortar; (c) thawing the fragments in sucrose mediu[redacted], free of divalent cations; (d) pressing the suspension of broken animals through a system of regularly spaced capillary constrictions of free organs; and (e) enrichment of glands by differential sedimentation and removal of contaminating material under a dissecting microscope. The nuclear isolation procedure is a large scale modification of a method previously described by Robert, using digitonin as a **non-ionic detergent** to solubilize cytoplasma and secretion without affecting the nuclear membrane. Nuclei obtained by this method show structural integrity and an unchanged chromosomal banding pattern. Their incorporation of UTP is within the same range as reported by other authors for nuclei by hand dissection.

8/3,AB/34 (Item 34 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03131173 77000339
Efficeint transcription of **RNA** into DNA by avian sarcoma virus polymerase.
Taylor JM; Illmensee R; Summers J
Biochimica et biophysica acta (NETHERLANDS) Sep 6 **1976**, 442 (3) p324-30, ISSN 0006-3002 Journal Code: A0W
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The DNAase digestion end-product of calf thymus DNA contains oligonucleotides that will function as primers for the efficient transcription into DNA of many naturally-occurring **RNA**'s by purified avian sarcoma virus **RNA** -directed DNA polymerase. The labeled DNA transcripts so obtained are valuable as probes for molecular hybridization studies. Typical applications of the method include the efficient transcription into DNA of 18 and 28 S rRNA as well as the **RNA**'s of avian sarcoma virus, polio virus, influenza virus, satellite tobacco necrosis virus and tobacco mosaic virus. In addition, when these primers are added to avian sarcoma virus particles that have been partially-disrupted with **non-ionic detergent** there is 6-fold stimulation of the endogenous **RNA**-directed DNA synthesis.

8/3,AB/35 (Item 35 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03124933 75190967
A morphological study of the internal component of influenza virus.
Almeida JD; Brand CM
Journal of general virology (ENGLAND) Jun **1975**, 27 (3) p313-8, ISSN 0022-1317 Journal Code: I9B
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Rapid treatment of influenza virus directly on the microscope grid with **non-ionic detergent** had allowed better visualization of the internal component. Many micrographs show that this ribonucleoprotein (RNP) is present as a continuous stand of 6 nm diam. arranged in the form of a double coil or helix. In spite of the minimal treatment to which the virus was subjected most helices still showed signs of degradation. The findings that we have obtained lead us to suggest that the RNP component of influenza virus must be very sensitive to both chemical and physical manipulations, any of which could cause it to fracture from one continuous strand into several pieces, although such breakages could possibly occur at specific points along its length.

8/3,AB/36 (Item 36 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03095681 77095333
Simultaneous staining of ribonucleic and deoxyribonucleic acids in unfixed cells using acridine orange in a flow cytofluorometric system.
Traganos F; Darzynkiewicz Z; Sharpless T; Melamed MR
journal of histochemistry and cytochemistry (UNITED STATES) Jan **1977**, 25 (1) p46-56, ISSN 0022-1554 Journal Code: IDZ
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Simultaneous staining of deoxyribonucleic (DNA) and ribonucleic acid (**RNA**) in nonfixed, but permeable, cells is described. Cells are made permeable by treatment with **non-ionic detergent** at low pH. **RNA** is denatured prior to, or during staining, by exposure of cells to chelating agents to ensure that DNA (native) and **RNA** (dentured) may be stained differentially with the metachromatic dye, acridine orange. The fluorescence of individual cells is measured in a flow cytofluorometer. A comparison between various staining procedures employing acridine orange or other intercalating dyes in uhfixed cells is discussed in terms of staining specificity, cell permeability and preservation. Evidence is provided that acridine orange staining of unfixed cells may be used as a simple, fast means of obtaining information on cell ploidy levels and cell cycle status from DNA measurements (green fluorescence), and cell transcriptional activity from **RNA** staining (red fluorescence), in human and murine cells lines, peripheral blood and bone marrow specimens from patients with leukemia and mitogenically (phytohemagglutinin) or antigenically (mixed lymphocyte culture) stimulated human peripheral blood cultures. Exposure of cells to detergent at low pH as an alternative to cell fixation or hypotonic treatment is proposed as a fast, convenient method of making cells permeable to dyes.

8/3,AB/37 (Item 37 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03032003 80115885
Electron-microscopy of intact nuclear DNA from human cells.
McCready SJ; Akrigg A; Cook PR
Journal of cell science (ENGLAND) Oct **1979**, 39 p53-62, ISSN 0021-9533 Journal Code: HNK
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Structures retaining many of the morphological features of nuclei may be released by lysing human cells in a **non-ionic detergent** and 2 M NaCl. Such nucleoids contain all the nuclear DNA packaged within a flexible cage of **RNA** and protein. HeLa nucleoids have been spread at an air-water interface and viewed in the electron microscope. A tangled network of superhelical fibres surrounds the collapsed cage. Irradiation with gamma-rays abolishes supercoiling and treatment with the untwisting enzyme or a low concentration of ethidium reduces it. A high concentration of ethidium induces supertwisting. The nuclear DNA of higher cells can be isolated naked, supercoiled and intact.

8/3,AB/38 (Item 38 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02984114 76111870
Initiation factors in protein synthesis by free and membrane-bound polyribosomes of liver and hepatoma.
Murty CN; Verney E; Sidransky H

Biochemical Journal (ENGLAND) Oct **1975**, 152 (1) p43-51, ISSN 0006-2936 Journal Co[redacted] 9YO
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The activity of initiation factors obtained from free and membrane-bound polyribosomes of liver and of transplantable H5123 hepatoma of rats was investigated by using an assay of protein synthesis in vitro in which poly (U)-directed polyphenylalanine synthesis was measured. Initiation factors of membrane-bound polyribosomes prepared by using the anionic detergent deoxycholate exhibited less activity in incorporating [14C]phenylalanyltRNA into polypetides than did initiation factors of free polyribosomes. However, when membrane-bound polyribosomes were prepared after using the **non-ionic detergent** Triton X-100, no significant differences in activities in polyphenylalanine synthesis were observed between the initiation factors of free and membrane-bound polyribosomes. These results suggest that Triton X-100 is preferable to deoxycholate in the isolation of of initiation factors from polyribosomes. Initiation factors, prepared by using Triton X-100, of free polyribosomes of hepatoma exhibited greater activity in the stimulation of polyphenylalanine synthesis than did the initiation factors of free or membrane-bound polyribosomes of host livers or of membrane-bound polyribosomes of hepatomas.

8/3,AB/39 (Item 39 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02938999 80096030
Comparison of the structural properties of Sindbis and Semliki forest virus nucleocapsids.
Soderlund H; von Bonsdorff CH; Ulmanen I
Journal of general virology (ENGLAND) Oct **1979**, 45 (1) p15-26, ISSN 0022-1317 Journal Code: I9B
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The envelope spikes of Sindbis and Semliki Forest virus are arranged in a T = 4 icosahedral surface lattice and, by deduction, it has been suggested that the nucleocapsid proteins are similarly arranged. After treatment of the virions with a **non-ionic detergent** the released nucleocapsids sediment in sucrose gradients at about 160S and 150S and have densities in CsCl of 1.42 g/ml and 1.425 g/ml, respectively, for Sindbis and Semliki Forest virus. At pH 6.0 Sindbis nucleocapsids do not contract like those of Semliki Forest virus. Nucleocapsids of both viruses are sensitive to the action of ribonuclease but only those of Semliki Forest virus undergo a drastic structural rearrangement due to the treatment. EDTA treatment in hypotonic conditions results in a decrease in the S-value for both particles. Electron micrographs show that the SFV nucleocapsids are partly 'unfolded' while those of Sindbis appear slightly contracted after exposure to EDTA.

8/3,AB/40 (Item 40 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02911775 78015285
Flow microfluorometric analysis of nuclear DNA in cells from solid tumors and cell suspensions. A new method for rapid isolation and straining of nuclei.
Vindelov LL
Virchows Archiv. B: Cell pathology (GERMANY, WEST) Aug 10 **1977**, 24 (3) p227-42, ISSN 0340-6075 Journal Code: XD5
Languages: ENGLISH
Document type: JOURNAL ARTICLE

microfluorometric DNA analysis is described. The membranes of the cells were lysed by the **non-ionic detergent** Nonidet P40. Single-cell suspensions, and specimens of solid tissues obtained with fine-needle biopsy, could be prepared equally well as the nuclei of solid tissue cells were released separately. Lysis was performed in the staining solution containing either ethidium bromide or propidium iodide. Fluorescence due to fluorochrome binding to **RNA** , was abolished instantaneously by the presence of **RNA**-se, and fluorochrome binding to secondary binding sites in DNA was inhibited with NaCl. The preparation time was 10 min and the samples were stable for a minimum of 12 h. With the basic version of the method, usable, but not always optimal, results were obtained in all the cell types tested: four different mouse ascites tumors, leucocytes, bone-marrow, liver cells, human lymphomas, human carcinomas of the breast and lung, mouse mammary carcinoma and solid JB-1 tumor. The method was further optimized for the JB-1 ascites tumour. The resulting two modified techniques are described. Differences in the staining of leucocytes with the analogues ethidium bromide and propidium iodide were demonstrated.

8/3,AB/41 (Item 41 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02862331 78178363

RNA -protein cross-linking in Eschericia coli 30S ribosomal subunits: a method for the direct analysis of the **RNA** regions involved in the cross-links.

Zwieb C; Brimacombe R

Nucleic acids research (ENGLAND) Apr **1978**, 5 (4) p1189-206, ISSN 0301-5610 Journal Code: O8L

Languages: ENGLISH

Document type: JOURNAL ARTICLE

A prerequisite for topographical studies on ribosomal subunits involving **RNA**-protein cross-linking is that the cross-linking sites on the **RNA** should be determined. Methodology is presented which offers a solution to this problem, using as a test system 30S subunits in which protein S7 has been cross-linked to the 16S **RNA** by ultraviolet irradiation. The method is based on a gel separation system in the presence of a **non-ionic detergent** . When a ribonucleoprotein fragment containing **RNA** -protein cross-links is applied to this system, non-cross-linked protein is removed, and simultaneously the cross-linked **RNA**-protein complex is separated from non-cross-linked **RNA**. Oligonucleotide analysis of the S7-**RNA** complex isolated in this manner showed it to consist of a region of **RNA** from sections P-A of the 16S **RNA**. A single characteristic oligonucleotide was absent from this region, and it was tentatively concluded that this missing oligonucleotide contains the actual site of cross-linking.

8/3,AB/42 (Item 42 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02657566 79232749

[Interaction of rat liver dexamethasone-receptor complexes with DNA]

Kharakteristika vzaimodeistviia deksametazon-retseptornykh kompleksov pecheni krys s DNK.

Romanova NA; Romanova GA; Rozen VB; Vaniushin BF

Biokhimiia (USSR) Mar **1979**, 44 (3) p529-42, ISSN 0006-307X Journal Code: A28

Languages: RUSSIAN Summary Languages: ENGLISH

Document type: JOURNAL ARTICLE ; English Abstract

Rat liver glucocorticoid-receptor complexes (GRC) acquire the ability to

bind to DNA in a high affinity manner after activation by heating or precipitation with (NH4)2SO4. DNA is practically non-saturable by GRC in low salt buffers as well as in 0.15 M NaCl-containing buffer, although in the latter case the binding decreases approximately 3--5 times. GRC bind to homo- and heterologous prokaryotic DNA in a similar way; in both cases an addition of KCl (up to 0.15 M) to the medium is followed by the same decrease of the binding. This data suggest that the association of GRC with DNA observed in vitro is not accompanied by "recognition" of any certain DNA site. Besides DNA, activated GRC can associate with other polymers, charged positively (DEAE-cellulose) or negatively (**RNA**, polyvinylsulfate). GRC interact very weakly with neutral compounds of the cellulose type but are strongly adsorbed on hydroxyapatite. Hence the activated GRC can be considered as an amphoteric protein. Salt solutions provoke dissociation of the GRC-DNA triple complexes: a complete dissociation is observed in the presence of 0,4 M NaCl or 0,4 M sodium phosphate buffer (pH 6,9). Sodium phosphate buffer also elutes GRC from other sorbents such as DEAE-cellulose or hydroxyapatite. No significant dissociation of the GRC-DNA complexes is observed at sucrose concentration up to 2 M. The data obtained are indicative of an essential role of electrostatic forces for the interaction of GRC with DNA. The **non-ionic detergent** Triton X-100 at a concentration as low as 0,05% completely destroys the GRC-DNA triple complexes. The models explicating the selectivity of the genome activation by GRC without their "recognition" of any specific DNA sequences are proposed.

8/3,AB/43 (Item 43 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02512812 78171697
Supercoiling of DNA and nuclear conformation during the cell-cycle.
Warren AC; Cook PR
Journal of cell science (ENGLAND) Apr **1978**, 30 p211-26, ISSN 0021-9533 Journal Code: HNK
Languages: ENGLISH
Document type: JOURNAL ARTICLE
When cells are lysed in solutions containing high concentrations of salt and a **non-ionic detergent**, structures are released which retain many of the morphological features of nuclei. These nucleoids contain superhelical DNA but are depleted of nuclear protein. We have analysed DNA conformation in nucleoids derived from HeLa cells synchronized at different stages in the cell cycle. The gross differences in nuclear morphology seen during the cell cycle are reflected in the morphology of the nucleoids; for example, the individual chromosomes of mitotic cells remain identifiable and aggregated within the mitotic nucleoid. The sedimentation rate of nucleoids in sucrose gradients reflects the gross nuclear morphology; the small S-phase nucleoids sediment 9 times faster than the large mitotic nucleoids. Despite these large differences at the gross level of organization, both the degree of supercoiling and the size of the units in which supercoiling is maintained are roughly similar in the nucleoids derived from cells in the different phases. The protein content of the various nucleoids is also very similar. Like the nucleoids made from randomly growing cultures of cells, mitotic nucleoids are excellent templates for the **RNA** polymerase of Escherichia coli.

8/3,AB/44 (Item 44 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02089222 76111463
Structural polypeptides of California encephalitis virus: BFS-283.
White AB
Archives of virology (AUSTRIA) **1975**, 49 (2-3) p281-90,

Journal Code: 8L7
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The polypepetides of California encephalitis virus (BFS-283) were analyzed by polyacrylamide gel electrophoresis (PAGE). Four polypeptides were detected in virions grown in both BHK-21 and LLC-MK2 cell cultures with molecular weights of 17,500. 30,000, 38,000, and 82,000 (VP-1, VP-2, VP-3, and VP-4, respectively). Viral proteins 2, 3, and 4 were glycoproteins and appeared to be associated with the envelope of the virus. Treatment of virions (rho=1.18 g/cm3) with then **non-ionic detergent**, NP-40, allowed detection of a **RNA**-rich fraction (rho=1.26/cm3) with contained the smallest polypeptides (VP-1).

8/3,AB/45 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09128420 BIOSIS NO.: 199497136790
Co-localization of polysomes, cytoskeleton, and membranes with protein bodies from corn endosperm: Evidence from fluorescence microscopy.
AUTHOR: Stankovic B; Abe S; Davies E(a)
AUTHOR ADDRESS: (a)Sch. Biol. Sci., Univ. Nebraska, Lincoln, NE 68588-0118 **USA
JOURNAL: Protoplasma 177 (1-2):p66-72 **1993**
ISSN: 0033-183X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Frozen corn endosperm was homogenized in a cytoskeleton-stabilizing buffer and stained directly (without pelleting) with rhodamine-phalloidin for actin and either thiazole orange to stain **RNA** or DiOC-6 to stain membranes prior to examination under the fluorescence microscope. Other samples were treated with a nonionic detergent alone or in conjunction with a ionic detergent prior to staining and fluorescence microscopy. Very gentle homogenization in unsupplemented buffer yielded a massive aggregate containing protein bodies that fluoresced after treatment with the ER stain DiOC-6. This aggregate was capped by an aggregate of unstained starch grains. More vigorous homogenization yielded more disperse patterns showing almost identical co-localization of ER, actin and **RNA** (polysomes). Homogenization in buffer plus **non-ionic detergent** removed most of the membrane yet maintained co-localization of actin and polysomes, while homogenization in double detergent removed the last traces of membrane and actin, and released over 70% of the polysomes. We interpret these results to suggest that protein bodies are surrounded by membranes, cytoskeleton and **RNA** (polysomes) and that the majority of the polysomes are attached more firmly to the cytoskeleton than to the membrane. This provides evidence from fluorescence microscopy to supplement that from biochemical analyses for the existence of cytomatrix-bound polysomes in plants.

1993

8/3,AB/46 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08896100 BIOSIS NO.: 199396047601
A tightly membrane-associated subpopulation of spectrin is tritiated palmitoylated.
AUTHOR: Mariani Mariagabriella; Maretzki Dieter; Lutz Hans U(a)
AUTHOR ADDRESS: (a)Lab. Biochem., ETH-Zentrum, Ch 8092 Zurich**Switzerland

JOURNAL: Journal of Biological Chemistry 268 (17):p12996-13001 1993
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A tightly membrane-associated form of spectrin (TMA-spectrin) was labeled when human red blood cells were incubated with (3H)palmitic acid. About 90% of spectrin was not fatty acid-acylated and was extracted from membranes by low salt buffers. The 3H-palmitoylated TMA-spectrin, however, resisted low and even high salt extraction and remained associated with inside-out vesicles that were generated in the process of spectrin-actin extraction from membranes. TMA-spectrin was preferentially extracted from KClstripped vesicles by 5 m urea at low ionic strength. TMA-spectrin was purified by gel filtration and by ion exchange chromatography in the presence of urea and a **non-ionic detergent**. Purified TMA-spectrin was 3H-palmitoylated exclusively in the beta subunit to 0.28 mol/mol after a 12-h incubation of red cells. The labeled palmitate may be bound as an ester or thioester, since hydroxylamine (1 M, pH 7.5) released the label completely. Peptide maps of 3H-palmitoylated TMA-spectrin showed three or two labeled peptides from the 6 subunit, when generated by V8 protease and trypsin, respectively. Two types of antibodies to spectrin reacted with purified TMA-spectrin, and TMA-spectrin contained the same antigenic peptides as low salt-extractable spectrin. Rabbit anti-ankyrin antibodies did not bind to TMA-spectrin. The substoichiometric incorporation of (3H)palmitic acid into TMA-spectrin could result from the slow turnover of endogenously bound fatty acids. Generation of the tightly membrane-associated and 3H-palmitoylated subpopulation of spectrin cannot be due to entrapment of an unmodified residual fraction of spectrin in right-side-out vesicles. Instead, the data suggest the existence of a subpopulation of spectrin molecules that undergo a covalent fatty acid modification and thereby alter their binding properties. This may offer a new, metabolically dependent mechanism for dynamic interactions between spectrin and the membrane lipid bilayer.

1993

8/3,AB/47 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07996030 BIOSIS NO.: 000093051703
SOLUBLE AND MEMBRANE-BOUND FORMS OF DOPAMINE BETA-HYDROXYLASE ARE ENCODED BY THE SAME MRNA
AUTHOR: LEWIS E J; ASNANI L P
AUTHOR ADDRESS: DEP. BIOCHEM. MOL. BIOL., OREGON HEALTH SCI. UNIV., PORTLAND, OREG. 97212-3098.
JOURNAL: J BIOL CHEM 267 (1). 1992. 494-500. **1992**
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A full length cDNA clone for bovine dopamine .beta.-hydroxylase was expressed in rat pheochromocytoma PC12 cells by stable transformation of this cell line with a plasmid expression vector. The recombinant protein exhibited dopamine .beta.-hydroxylase enzyme activity and was found in both the soluble and membrane fractions of the secretory vesicle. Immunoprecipitation of cell extracts from recombinant cell lines with dopamine .beta.-hydroxylase antisera followed by fractionation on sodium dodecyl sulfate-polyacrylamide gel electrophoresis revealed two subunits, which migrated to relative molecular masses of 76 and 78 kDa. The recombinant protein co-fractionated with neurotransmitter when

[illegible] were separated by sucrose gradient density centrifugation, suggesting that the protein was routed to the secretory vesicles. Dopamine .beta.-hydroxylase immunoreactivity in those sucrose gradient fractions presumed to contain secretory vesicles was resistant to treatment with trypsin unless the **non-ionic detergent** Triton X-100 was also present to disrupt membrane structure. The 76- and 78-kDa isoform were each found in both the membrane and soluble fractions of the secretory vesicle. Treatment of cultured cells with nerve growth factor or 8-(4-chlorophenylthio)-cyclic AMP alters the relative distribution of the subunits such that the 76-kDa form predominates. The subcellular distribution of a dopamine .beta.-hydroxylase cDNA clone lacking the first 16 nucleotide residues was also determined. The predicted amino acid sequence of the protein encoded by this cDNA would be deleted of the first 13 residues of the signal sequence, which were reported to be present in the membrane-bound form, but not the soluble form, of native dopamine .beta.-hydroxylase (Taljanidisz, J., Stewart, L., Smith, A. J., and Klinman, J. P. (1989) Biochemistry 28, 10054-10061). Immunoprecipitable dopamine .beta.-hydroxylase derived from expression of the deleted cDNA was found in both the membrane-bound and soluble fractions of the secretory vesicle. These experiments demonstrate that the membrane-bound and soluble forms of dopamine .beta.-hydroxylase are derived from one primary translation product, which is also sufficient to produce enzyme activity. In addition, the amino-terminal amino acids encoding residues 1-13, which compose the hydrophilic region of the signal sequence, are not necessary for the biogenesis of membrane-bound dopamine .beta.-hydroxylase.

1992

8/3,AB/48 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05662664 BIOSIS NO.: 000084011069
PHYSICOCHEMICAL CHARACTERIZATION OF FESTUCA LEAF STREAK VIRUS
AUTHOR: LUNDSGAARD T
AUTHOR ADDRESS: DEP. PLANT PATHOLOGY, THE ROYAL VETERINARY AND AGRIC. UNIV., THORVALDSENSVEJ 40, 1871 FREDERIKSBERG C., DENMARK.
JOURNAL: J GEN VIROL 68 (3). 1987. 931-936. **1987**
FULL JOURNAL NAME: Journal of General Virology
CODEN: JGVIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Particles of festuca leaf streak virus (FLSV) contain three major proteins. One of these [mol. wt. 49,000 (49K)] is the main constituent of the nucleocapsid, whereas the other two (mol. wt. 58K and 20K) were released from the nucleocapsid when particles were treated with **non-ionic detergent**. The 58K protein is glycosylated. The 58K, 49K and 20K proteins correspond to the G, N and M proteins of rhabdoviruses, respectively. Four minor proteins associated with the virus particles have mol. wt. of 189K, 117K, 101K and 41K. The 189K and 101K proteins are associated with the nucleocapsid, whereas the 117K protein was found in the soluble fraction after detergent treatment. Nucleic acid isolated from virus particles is probably **RNA** with an estimated mol. wt. of 4.3 .times. 106. The buoyant density of virus particles in sucrose was estimated to be 1.194 g/ml and the s20,w to be 704S. The present results, together with previous information, make FLSV a definitive member of subgroup A of the plant rhabdovirus group of the family Rhabdoviridae.

1987

8/3,AB/49 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05116756 BIOSIS NO.: 000081074880
A DISAPPEARANCE OF A 24-KILODALTON ACID-SOLUBLE PROTEIN FROM LIVER CHROMATIN OF NORMAL AND STARVED HENS FOLLOWING D GALACTOSAMINE ADMINISTRATION
AUTHOR: PALYGA J
AUTHOR ADDRESS: DEP. GENETICS, EDUCATIONAL UNIV. KIELCE, REWOLUCJI PAZDZIERNIKOWEJ 33; 25-518 KIELCE, POLAND.
JOURNAL: Z NATURFORSCH SECT C BIOSCI 40 (11-12). 1985 (RECD. 1986). 798-805. **1985**
FULL JOURNAL NAME: Zeitschrift fuer Naturforschung Section C Biosciences
CODEN: ZNCBD
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Normal and starved adult chickens were injected intraperitoneally with D-galactosamine hydrochloride (0.5 g/kg body weight) and 6 h later liver chromatin acid-soluble proteins were isolated. These proteins were resolved by a two-dimensional polyacrylamide gel electrophoresis in the presence of **non-ionic detergent**. Triton X-100, in the first dimension and aniomic detergent, sodium dodecyl sulfate, in the second dimension. Although spotting patterns of acid-soluble chromatin proteins were remarkedly similar between normal and starved control birds and those receiving D-galactosamine, a disappearance of a 24-kDa protein after administration of this agent was found. Moreover, it was shown that this protein was also completely absent in the chicken erytrocyte chromatin which was known to be inactive in **RNA** synthesis. It seems that the disappearance of the 24-kDa chromatin protein may be associated with inhibiting of transcripting of transcription in hen liver after D-galactosamine administration and during hen erythrocyte maturation.

1985

8/3,AB/50 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

03667493 BIOSIS NO.: 000074083070
CONFORMATIONAL CHANGES INDUCED BY SALT IN COMPLEXES OF HISTONES AND SUPER HELICAL NUCLEAR DNA
AUTHOR: LEVIN J M; COOK P R
AUTHOR ADDRESS: SIR WILLIAM DUNN SCH. PATHOL., UNIV. OXFORD, SOUTH PARKS ROAD, OXFORD.
JOURNAL: J CELL SCI 50 (0). 1981. 199-208. **1981**
FULL JOURNAL NAME: Journal of Cell Science
CODEN: JNCSA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: When [human cervical carcinoma] HeLa cells are lysed in a **non-ionic detergent** and 0.75 M NaCl, structures are released that retain many of the morphological features of nuclei. These nucleoids contain intact nuclear DNA and the core histones which dissociate on raising the salt concentration. The structure of these complexes was probed using 2 agents that can detect free energy of supercoiling ethidium and **RNA** polymerase. Negative supercoiling can be detected by **RNA** polymerase in 0.2 M NaCl but not by ethidium below 0.92 M NaCl.

1981

8/3,AB/51 (Item 7 [redacted]om file: 5)
DIALOG(R)File 5:Biosis Previews(R)

03658713 BIOSIS NO.: 000074074290
EFFECT OF TREATMENT WITH TRITON X-100 ON DNA INTEGRITY AND ON DNA TO **RNA** TO PROTEIN RATIO OF RAT LIVER NUCLEI
AUTHOR: CARLO P; MARTELLI A; BIGNONE F A
AUTHOR ADDRESS: IST. FARMACOL., UNIV. GENOVA.
JOURNAL: BOLL SOC ITAL BIOL SPER 57 (22). 1981 (RECD. 1982). 2203-2208. **1981**
FULL JOURNAL NAME: Bollettino della Societa Italiana di Biologia Sperimentale
CODEN: BSIBA
RECORD TYPE: Abstract
LANGUAGE: ITALIAN

ABSTRACT: A procedure is described that gives clean nuclei with intact DNA from a rat liver cell suspension. Cytoplasmic contamination is reduced by successive treatments with a **non-ionic detergent**, Triton X-100 (0.75%). With the ratios DNA:**RNA**:protein of 1:0.09:3.29 (2 Triton X-100 steps), the integrity of DNA is preserved. Further decrease in **RNA** and protein content (3 Triton -100 steps) causes DNA breakage, probably because of extraction of nuclear proteins. To estimate DNA integrity, its viscosity was determined by the use of a new oscillating cruicile viscometer; this method makes possible the evaluation of extremely small levels of DNA damage induced by 0.067 mg/kg body weight of dimethylnitrosamine injected i.p.

1981

8/3,AB/52 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

03620830 BIOSIS NO.: 000074036407
REVERSE TRANSCRIPTASE EC-2.7.7.7 ASSOCIATED WITH AVIAN SARCOMA LEUKOSIS VIRUSES 1. COMPARISON OF INTRA VIRION CONTENT OF MULTIPLE ENZYME FORMS
AUTHOR: UENO A; ISHIHAMA A; TOYOSHIMA K
AUTHOR ADDRESS: INST. VIRUS RES., KYOTO UNIV., SAKYO-KU, KYOTO, KYOTO 606.
JOURNAL: J BIOCHEM (TOKYO) 91 (1). 1982. 311-322. **1982**
FULL JOURNAL NAME: Journal of Biochemistry (Tokyo)
CODEN: JOBIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: **RNA**-dependent DNA polymerase (reverse transcriptase) was solubilized from 3 related strains of avian sarcoma virus (ASV B77, ASV tsLA334 and ASV QV2) and avian myeloblastosis virus (AMV) and a chicken endogenous virus, Rous-associated virus type O (RAV-O), by a combination of **non-ionic detergent** treatment and CsCl step-gradient centrifugation and was subsequently separated into individual enzyme forms by poly(C)-agarose column chromatography. The newly developed 2-step method purified the 3 molecular forms (.alpha.-, .alpha..beta.- and .beta.-form) of highly active enzyme rapidly and quantitatively from all the 5 virus strains examined. The molar ratio of the 3 enzyme forms differed among the virus strains. For the 3 sarcoma viruses, the major species was the .alpha..beta.-form enzyme, the putative holoenzyme; the .alpha. and .beta.-form enzymes were less than a few percent and 15-25%, respectively. The .alpha.-form enzyme content was higher for the 2 leukosis viruses than for the 3 sarcoma viruses. Both the total DNA polymerase activity and the content of the 2 enzyme subunits in purified virions of the 3 sarcoma viruses was in the following order: ASV tsLA334

> ASV B77 > ASV QV2, which paralleled the virus yield at a permissive temperature in roller bottle cultures of chick embryo fibroblasts. No alteration was found in the thermolability of DNA polymerases between tsLA334, which carries temperature sensitive mutations affecting virus growth and cell-transformation, and other viruses.

1982

8/3,AB/53 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

03196662 BIOSIS NO.: 000071009773
IN-VITRO SYNTHESIS OF **RNA** BY DISSOCIATED LETTUCE NECROTIC YELLOWS VIRUS PARTICLES
AUTHOR: TORIYAMA S; PETERS D
AUTHOR ADDRESS: LAB. VIROL., AGRIC. UNIV., BINNENHAVEN 11, 6709 PD WAGENINGEN, NETH.
JOURNAL: J GEN VIROL 50 (1). 1980. 125-134. **1980**
FULL JOURNAL NAME: Journal of General Virology
CODEN: JGVIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The presence of an endogenous transcriptase in purified lettuce necrotic yellows virus (LNYV) particles was confirmed. The enzyme requires a temperature of 22.degree. C, a pH value of 7.7, a detergent and Mg2+ concentration of 0.025% and 4 mM, respectively, for maximal synthesis of **RNA**; Zn2+, Ca2+ or Mn2+ inhibited the activity. The chelating agents EDTA and ethyleneglycolbis(2-aminoethylether)tetra-acetic acid (EGTA) stimulated the reaction, and in their presence the optimal Mg2+ concentration was higher. The in vitro transcription products of LNYV hybridized to the virus genome. After treatment of the virus with a **non-ionic detergent** the transcription complex could be separated by gradient centrifugation into 2 inactive fractions, the pellet and the upper part of the gradient. The activity could be restored by combining the 2 fractions.

1980

8/3,AB/54 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02939940 BIOSIS NO.: 000069048058
DISSOCIATION OF TICK-BORNE ENCEPHALITIS VIRUS BY TRITON X-100 AND CETYLTRIMETHYL AMMONIUM BROMIDE
AUTHOR: HEINZ F; KUNZ C
AUTHOR ADDRESS: INST. VIROL., UNIV. VIENNA, A-1095 VIENNA, AUSTRIA.
JOURNAL: ACTA VIROL (PRAGUE) (ENGL ED) 23 (3). 1979. 189-197. **1979**
FULL JOURNAL NAME: Acta Virologica (PRAGUE) (English Edition)
CODEN: AVIRA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The uses of the **non-ionic detergent** Triton X-100 (TX-100) and cationic cetyltrimethylammonium bromide (CTAB) for production of tick-borne encephalitis (TBE) virus subunits were compared. TX-100 split the virus into hemagglutinating envelope components which contain the virion proteins V3 and V1 and into a lipid-free nucleoprotein composed of **RNA** and V2. The lipid content of released envelope fragments decreased with increasing detergent concentration. By the use

of CTAB, the viral glycoprotein V3 could be prepared [redacted]
electrophoretically pure and active, i.e., hemagglutinating, form.
1979

8/3,AB/55 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02912478 BIOSIS NO.: 000069020594
IN-VIVO AND IN-VITRO PHOSPHORYLATION OF MURINE MAMMARY TUMOR VIRUS PROTEINS
AUTHOR: DION A S; FOUT G S; POMENTI A A
AUTHOR ADDRESS: DEP. MOL. BIOL., INST. MED. RES., COPEWOOD ST., CAMDEN, N.J. 08103, USA.
JOURNAL: J GEN VIROL 44 (3). 1979. 669-678. **1979**
FULL JOURNAL NAME: Journal of General Virology
CODEN: JGVIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A comparative study of in vitro and in vivo phosphorylation of murine mammary tumor virus, a type B **RNA** virus, is reported. The protein kinase activity associated with murine mammary tumor virus catalyzed the in vitro phosphorylation of endogenous virus polypeptides. This kinase activity required a divalent metal cation, a **non-ionic detergent**, and was stimulated in the presence of dithiothreitol. Exogenous cyclic[c]AMP was not required. The 32P-labeled products of the in vitro reaction were completely sensitive to Pronase digestion and the phosphate was attached mainly by phosphomonoester linkage to serine residues. As determined by SDS[sodium dodecyl sulfate]-polyacrylamide gel electrophoresis, heterogeneous labeling of major and minor virus polypeptides was observed under in vitro conditions. The in vivo labeling of type B virus produced by a continuous cell line (MuMT-73), established from pooled mammary adenocarcinomas of Balb/cfC3H mice, demonstrated specific phosphoproteins associated with murine mammary tumor virus. The major phosphorylated proteins had MW of 18,000 and 12,000 (p18 and p12) after isolation by molecular sieving chromatography and analysis by gel electrophoresis.

1979

8/3,AB/56 (Item 12 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02898757 BIOSIS NO.: 000069006873
THE INTERFERENCE OF CYTOPLASMIC MEMBRANE BOUND MATERIAL FROM PLANT CELLS WITH THE DETECTION OF A PLANT RHABDOVIRUS TRANSCRIPTASE
AUTHOR: FRANCKI R I; PETERS D
AUTHOR ADDRESS: DEP. PLANT PATHOL., WAITE AGRIC. RES. INST., UNIV. ADELAIDE, S. AUST., AUST.
JOURNAL: J GEN VIROL 41 (3). 1978. 467-478. **1978**
FULL JOURNAL NAME: Journal of General Virology
CODEN: JGVIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Nuclei and chloroplasts isolated from cell-free extracts of Nicotiana glutinosa L. leaves by sedimentation at 1000 g contain DNA-directed **RNA** polymerase activity. Whereas only traces of **RNA** polymerase activity were detected in fractions prepared from the 1000 g supernatant of healthy leaf extracts, **RNA**-directed **RNA** polymerase was readily detected in similar extracts from lettuce necrotic yellows virus (LNYV)-infected plants. This

virus-associated enzyme activity was strongly inhibited by fractions containing membrane material from ruptured leaf cells of both healthy and virus-infected plants. Fractions with LNYV-associated **RNA** polymerase activity were prepared after treating the 1000 g supernatant with the **non-ionic detergent** Nonidet P-40. **RNA** polymerase activities both of cell-free leaf extract fractions and of purified LNYV preparations were rapidly lost during storage: loss of activity was more rapid in the presence of the detergent. Results presented in the paper are discussed in relation to the difficulties encountered in demonstrating **RNA** transcriptase activity associated with purified rhabdovirus preparations. To detect such enzymes it is necessary to use rapid procedures to obtain virus preparations free of contaminating cellular membranes.

1978

8/3,AB/57 (Item 13 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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02894305 BIOSIS NO.: 000069002421
EFFECT OF VIRAL RNASE H ON THE AVIAN SARCOMA VIRAL GENOME DURING EARLY TRANSCRIPTION IN-VITRO
AUTHOR: FRIEDRICH R; MOELLING K
AUTHOR ADDRESS: INST. TUMORIMMUNOL., UNIV. FREIB., D-7800 FREIBURG IM BREISGAU, W. GER.
JOURNAL: J VIROL 31 (3). 1979. 630-638. **1979**
FULL JOURNAL NAME: Journal of Virology
CODEN: JOVIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The influence of viral RNase H on the transcription of the avian sarcoma virus **RNA** in a virion-associated reaction was investigated. The ability of RNase H to degrade the **RNA** moiety of the initially formed **RNA**-DNA hybrid at the 5' end of the viral genome was greatly dependent on the exact concentration of **non-ionic detergent** used to activate the reaction. At a detergent concentration optimal for extensive and faithful in vitro transcription of avian sarcoma virus **RNA** by the virion-associated **RNA** -dependent DNA polymerase, most of the 5' terminus of the **RNA** was digested in 30 min at 41.degree. C. At higher than optimal detergent concentrations, little of that **RNA** was digested. Removal of the 5'-terminal redundancy in the **RNA** after its transcription into DNA is a prerequisite for base pairing of the DNA to the 3'-terminal redundant sequence. Lack of removal of this sequence leads to incorrect elongation and substantial reduction of DNA synthesis. When tested with a synthetic **RNA**-DNA hybrid, virion-associated RNase H did not reveal a detergent dependence.

1979

8/3,AB/58 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

02756022 BIOSIS NO.: 000068066629
CHARACTERISTICS OF THE INTERACTION OF RAT LIVER DEXAMETHASONE RECEPTOR COMPLEXES WITH DNA
AUTHOR: ROMANOVA N A; ROMANOV G A; ROZEN V B; VANYUSHIN B F
AUTHOR ADDRESS: LAB. ENDOCRINOL., BIOL. FAC., MOSC. STATE UNIV., MOSCOW, USSR.
JOURNAL: BIOKHIMIYA 44 (3). 1979. 529-542. **1979**

FULL JOURNAL NAME: Biokhimiya
CODEN: BIOHA
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

ABSTRACT: Rat liver glucocorticoid-receptor complexes (GRC) acquire the ability to bind to DNA in a high affinity manner after activation by heating or precipitation with (NH)2SO4. DNA is practically non-saturable by GRC in low salt buffers and in 0.15 M NaCl-containing buffer, although in the latter case the binding decreases approximately 3-5 times. GRC bind to homo- and heterologous prokaryotic DNA in a similar way; in both cases an addition of KCl (up to 0.15 M) to the medium is followed by the same decrease of the binding. The association of GRC with DNA observed in vitro is not accompanied by recognition of any certain DNA site. Besides DNA, activated GRC can associate with other polymers, charged positively (DEAE-cellulose) or negatively (**RNA**, polyvinylsulfate). GRC interact very weakly with neutral compounds of the cellulose type but are strongly adsorbed on hydroxyapatite. Hence the activated GRC can be considered as an amphoteric protein. Salt solutions provoke dissociation of the GRC-DNA triple complexes: a complete dissociation is observed in the presence of 0,4 M NaCl or 0,4 M sodium phosphate buffer (pH 6,9). Sodium phosphate buffer also elutes GRC from other sorbents such as DEAE-cellulose or hydroxyapatite. No significant dissociation of the GRC-DNA complexes is observed at sucrose concentration up to 2 M. Electrostatic forces may have an essential role in the interaction of GRC with DNA. The **non-ionic detergent** Triton X-100 at a concentration as low as 0.05% completely destroys the GRC-DNA triple complexes. Models explicating the selectivity of the genome activation by GRC without their recognition of any specific DNA sequences are proposed.

1979

8/3,AB/59 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02651846 BIOSIS NO.: 000067039910
ISOLATION AND PURIFICATION OF MYO TUBE AND MYO BLAST NUCLEI FROM CULTURES OF EMBRYONIC CHICK SKELETAL MUSCLE
AUTHOR: DAVID J D; FREDRICKSON R L; PETERSON G R
AUTHOR ADDRESS: UNIV. MO., COLUMBIA, MO. 65201, USA.
JOURNAL: EXP CELL RES 117 (1). 1978. 63-70. **1978**
FULL JOURNAL NAME: Experimental Cell Research
CODEN: ECREA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Methods are described for the preparation of purified myotubes from embryonic chick skeletal muscle cultures and the preparation of purified nuclei from both myotubes and myoblasts. Myotubes are released from the culture dish by digestion of their collagen substratum with collagenase, and purified by sucrose density gradient sedimentation. Nuclei are prepared from the isolated myotubes by controlled homogenization in Ca2+-free medium and sedimentation through 2.1 M sucrose. Nuclei are prepared from cultured myoblasts in a similar fashion, with the inclusion of the **non-ionic detergent** NP-40 in the homogenization medium and sedimentation through 2.4 M sucrose. Phase contrast microscopic examination showed that the nuclear preparations are free of visible cytoplasmic contamination, and are morphologically similar to nuclei observed in situ. Biochemical assays (protein/DNA and **RNA**/DNA ratios) confirm the purity of the nuclear preparations. Both nuclear preparations have been used to prepare purified chromatin which has spectral and chemical properties similar to those reported for chromatin purified directly from several chick

tissues.

1978

8/3,AB/60 (Item 16 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02373995 BIOSIS NO.: 000065031025
THE POLY PEPTIDES OF HEMAGGLUTINATING ENCEPHALOMYELITIS VIRUS AND ISOLATED SUB VIRAL PARTICLES
AUTHOR: POCOCK D H; GARWES D J
AUTHOR ADDRESS: MICROBIOL. DEP., INST. RES. ANIM. DIS., AGRIC. RES. COUNC., COMPTON, NEWBURY, BERKS., ENGL., UK.
JOURNAL: J GEN VIROL 37 (3). 1977 487-500. **1977**
FULL JOURNAL NAME: Journal of General Virology
CODEN: JGVIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Hemagglutinating encephalomyelitis virus (HEV), a member of the coronavirus group, was adapted for growth in adult pig thyroid cell cultures and purified by (NH4)2SO4 precipitation and rate zonal centrifugation through sucrose gradients. Polyacrylamide gel electrophoresis of samples of purified virus revealed the presence of 5 polypeptides, 4 of which contained carbohydrate. The MW of these proteins were 180,000 (gp 180), 125,000 (gp 125), 100,000 (gp 100), 56,000 (p 56) and 26,500 (gp 26.5). After treatment of the virus with the **non-ionic detergent** Nonidet P40, 2 subviral components were isolated. An **RNA**-containing particle, sedimenting in sucrose gradients at the same rate as untreated virus, was analyzed and contained 2 polypeptides, p 56 and gp 26.5. The 2nd complex sedimented at a much slower rate and contained 3 glycoproteins gp 180, gp 125 and gp 100. Comparison of these findings with data published for other members of the coronavirus group [transmissible gastroenteritis virus and infectious bronchitis virus] is discussed.

1977

8/3,AB/61 (Item 17 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02154899 BIOSIS NO.: 000063069904
SIMULTANEOUS STAINING OF **RNA** AND DNA IN UNFIXED CELLS USING ACRIDINE ORANGE IN A FLOW CYTO FLUOROMETRIC SYSTEM
AUTHOR: TRAGANOS F; DARZYNKIEWICZ Z; SHARPLESS T; MELAMED M R
JOURNAL: J HISTOCHEM CYTOCHEM 25 (1). 1977 46-56. **1977**
FULL JOURNAL NAME: Journal of Histochemistry and Cytochemistry
CODEN: JHCYA
RECORD TYPE: Abstract

ABSTRACT: Simultaneous staining of DNA and **RNA** in non-fixed, but permeable, cells is described. Cells are made permeable by treatment with **non-ionic detergent** at low pH. **RNA** is denatured prior to, or during staining, by exposure of cells to chelating agents to ensure that DNA (native) and **RNA** (denatured) may be stained differentially with the metachromatic dye, acridine orange. The fluorescence of individual cells is measured in a flow cytofluorometer. A comparison between various staining procedures employing acridine orange or other intercalating dyes in unfixed cells is discussed in terms of staining specificity, cell permeability and preservation. Evidence is provided that acridine orange staining of unfixed cells may be used as a

cell cycle status fr[redacted]DNA measurements (green fluore[redacted]nce), and cell transcriptional activity from **RNA** staining (red fluorescence), in human and murine cell lines, peripheral blood and bone marrow specimens from patients with leukemia and mitogenically (phytohemagglutinin) or antigenically (mixed lymphocyte culture) stimulated human peripheral blood cultures. Exposure of cells to detergent at low pH as an alternative to cell fixation or hypotonic treatment is proposed as a fast, convenient method of making cells permeable to dyes.

1977

8/3,AB/62 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02150749 BIOSIS NO.: 000063065752
DNA DEPENDENT AND **RNA** DEPENDENT DNA POLYMERASES PROGRESSIVE CHANGES IN RABBIT ENDOMETRIUM DURING PRE IMPLANTATION STAGE OF PREGNANCY
AUTHOR: YANG W-K; TYNDALL R L; DANIEL J C JR
JOURNAL: BIOL REPROD 15 (5). 1976 604-613. **1976**
FULL JOURNAL NAME: Biology of Reproduction
CODEN: BIREB
RECORD TYPE: Abstract

ABSTRACT: DNA polymerase activities were studied in rabbit endometria at estrus and through the first 7 days of pregnancy. Extracts of total endometrial homogenates by high salt gave 2 peaks of polymerase activity by sucrose gradient centrifugation; the 6-8S polymerase showed considerable increase in specific activity which reached a maximum at 5-7 days post-coitum but the 3-4S polymerase showed only a slight increase after 2 days of pregnancy. A 5-6S **RNA**-dependent DNA polymerase activity, extracted by combined use of hypertonic salt solution and **non-ionic detergent** from particulate subcellular functions, appeared in the endometrium after coitus, reached a maximum at day 3-4 and declined thereafter. This **RNA**-dependent DNA polymerase activity, isolated by phosphocellulose chromatography at distinct regions of salt gradient, showed preference for template-primers such as (rA)n.cntdot.(dT)9 and (rC)n.cntdot.(dG)6 but did not utilize 70S **RNA** of **RNA** tumor viruses. Attempts to demonstrate oncorna virus expression by other means have been unsuccessful with endometrium of 3 day pregnant rabbits. Interrelation between the changes of these DNA polymerase activities and the DNA replication in the endometrial cells is discussed.

1976

8/3,AB/63 (Item 19 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02124530 BIOSIS NO.: 000063039526
EFFICIENT TRANSCRIPTION OF **RNA** INTO DNA BY AVIAN SARCOMA VIRUS POLYMERASE
AUTHOR: TAYLOR J M; ILLMENSEE R; SUMMERS J
JOURNAL: BIOCHIM BIOPHYS ACTA 442 (3). 1976 324-330. **1976**
FULL JOURNAL NAME: Biochimica et Biophysica Acta
CODEN: BBACA
RECORD TYPE: Abstract

ABSTRACT: The DNAase digestion end-product of calf thymus DNA contains oligonucleotides that function as primers for the efficient transcription into DNA of many naturally-occurring **RNA** by purified avian sarcoma

obtained are valuable as probes for molecular hybridization studies. Typical applications of the method include the efficient transcription into DNA of 18 and 28 S rRNA [Drosophila melanogaster] and the RNA's of avian sarcoma virus, polio virus, influenza virus, satellite tobacco necrosis virus and tobacco mosaic virus. When these primers are added to avian sarcoma virus particles that were partially disrupted with non-ionic detergent, there is a 6-fold stimulation of

observed in [redacted] blastic crisis but not in the chronic phase. From the present study and a review of the published cases, it appears that the incidence of such a masked Ph1, which cannot be detected by conventional Giemsa staining, is < 0.6% in CML cases. The 1st and 2nd cases with a variant Ph1 translocation mentioned above, developed a myeloid blastic crisis after the induction of remission of a lymphoid blastic crisis. It is unclear whether the occurrence of such blast cells in the 2 cases and the cytogenetic findings are conicidental. The evidence supports the notion of lymphoid-myeloid multipotentiality of certain leukemic cells.

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? s rna and (isolat? or purif? or separat) and (blood or plasma or bone
marrow) and review

          560959  RNA
         1367573  ISOLAT?
          771076  PURIF?
               4  SEPARAT
         2609898  BLOOD
          739329  PLASMA
           62821  BONE MARROW
          462753  REVIEW
      S5      63  RNA AND (ISOLAT? OR PURIF? OR SEPARAT) AND (BLOOD OR
                  PLASMA OR BONE MARROW) AND REVIEW
? s s5 and kit

              63  S5
           17617  KIT
      S6       1  S5 AND KIT
? s l5 and (ph(w)6.5 or ph(w)7 or ph(w) 7.5 or ph(w) 8 or ph(w)8.5)

            5400  L5
         1527102  PH
               0  6.5
               0  PH(W)6.5
         1527102  PH
         1650787  7
           55350  PH(W)7
         1527102  PH
               0  7.5
               0  PH(W)7.5
         1527102  PH
         1483489  8
           19651  PH(W)8
         1527102  PH
               0  8.5
               0  PH(W)8.5
      S7      13  L5 AND (PH(W)6.5 OR PH(W)7 OR PH(W) 7.5 OR PH(W) 8 OR
                  PH(W)8.5)
? rd

...completed examining records
      S8      12  RD (unique items)
? t s8/3,ab/all


 8/3,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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07895212   94213839
  Base  pairing  and steric interactions between pyrimidine strand bridging
loops and the purine strand in DNA pyrimidine.purine.pyrimidine triplexes.
  Booher MA; Wang S; Kool ET
  Department of Chemistry, University of Rochester, New York 14627.
  Biochemistry (UNITED  STATES)  Apr 19 1994,  33  (15)  p4645-51,  ISSN
```

0006-2960 Journal Code: A0G
Contract/Grant No.: GM46625, GM, NIGMS
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Bimolecular triple-helical DNA complexes recently have found use in a new strategy for the recognition of single-stranded nucleic acids, in which circular (Kool, 1991; Prakash & Kool, 1992) or hairpin-shaped (Giovannangeli et al., 1991; D'Souza & Kool, 1992) oligonucleotides bind these single strands by triplex formation. Bimolecular triplexes may also be formed in vivo as H-DNA, where this structure may potentially play a role in gene expression and recombination (Belotserkovskii et al., 1990; Hanvey et al., 1989; Shimizu et al., 1989). In all of these complexes, the central strand of the triplex must pass beyond the loop that bridges the outer two strands, and models and preliminary experiments have indicated that there may be important interactions between this central strand and the loop (Prakash & Kool, 1992). We now report thermal denaturation studies carried out specifically to investigate these interactions in detail, using as a model the 5'-loop and 3'-loop complexes formed between 14 pyrimidine oligodeoxynucleotides having the sequence 5'-dTTCTTTTCL1TTTL5CTTTTCTT, where L1 and L5 represent varied nucleotides in the loop (which is underlined), and eight target strands having the sequence 5'-dCCCCFAAGAAAAG-3' or 5'-dGAAAAGAAFCCCCC-3', where F is a varied nucleotide flanking the triplex in the central strand. Results correlated from 64 different sequence combinations show that there is wide variation in the stabilities of the complexes, indicating specific and substantial interactions between the nucleotides at the L1, F, and L5 positions. Melting temperatures at pH 7.0 range from 17.0 degrees C to 34.6 degrees C, and free energies (37 degrees C) range from -3.2 to -7.8 kcal mol-1.(ABSTRACT TRUNCATED AT 250 WORDS)

8/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07895211 94213838

Stabilities of nucleotide loops bridging the pyrimidine strands in DNA pyrimidine.purine.pyrimidine triplexes: special stability of the CTTTG loop.

Wang S; Booher MA; Kool ET
Department of Chemistry, University of Rochester, New York 14627.

Biochemistry (UNITED STATES) Apr 19 1994, 33 (15) p4639-44, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: GM46625, GM, NIGMS
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Recent studies of DNA hairpin loops have shown considerable dependence of the stability on the sequence of the loop [Senior, M., Jones, R. A., & Breslauer, K. J. (1988a) Proc. Natl. Acad. Sci. U.S.A. 85, 6242-6246; Xodo, L. E., Manzini, G., Quadrifoglio, F., van der Marel, G., & van Boom, J. H. (1989) Biochimie 71, 793-803; Hirao, I., Nishimura, Y., Tagawa, Y., Watanabe, K., & Miura, K. (1992) Nucleic Acids Res. 20, 3891-3896]. Analogous studies have not, until now, been carried out with loops in triple helices. We report the results from experiments in which we examine the relative stabilities of pentanucleotide loops that bridge between the pyrimidine strands in DNA pyr.pur.pyr triple helices. There are two types of loops that are defined by the relative orientation of the purine strand: a 5'-loop and a 3'-loop. The sequences examined in this study are the bimolecular triplexes formed between 5'-dTTCTTTTCL1TTTL5CTTTTCTT (loop nucleotides are underlined, and L1 and L5 represent varied nucleotides) and the two purine strands, 5'-dAAGAAAAG-3' and 5'-dGAAAAGAA-3'. The first and last nucleotides in the loop are varied, since stacking interactions may be strongest at these positions [Senior et al., 1988a; Senior, M., Jones, R. A., & Breslauer, K. J. (1988b) Biochemistry 27, 3879-3885], and we examine 14 sequence combinations for

each loop type. Thermal denaturation studies carried out at pH 7.0 indicate considerable variation in the stabilities of these loops. (ABSTRACT TRUNCATED AT 250 WORDS)

8/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07384640 90283501
[The 5S rRNA-protein complex of Escherichia coli studied by carbodiimide modification]
Izuchenie 5S rRNK-belkovogo kompleksa Escherichia coli s pomoshch'iu modifikatsii karbodiimidom.
Dontsova OA; Efimov AV; Kopylov AM
Nauchnye Doki Vyss Shkoly Biol Nauki (USSR) 1990, (2) p22-30, ISSN 0470-4606 Journal Code: A3B
Languages: RUSSIAN Summary Languages: ENGLISH
Document type: JOURNAL ARTICLE English Abstract
5S rRNA-protein complex has been reconstituted from 5S rRNA and total protein of large (L) ribosomal subunit of Escherichia coli. The complex consists of 5S rRNA and 3 proteins only: L5 , L18, L25. A water-soluble carbodiimide [N-cyclohexyl-N'-(2-morpholinoethyl)-carbodiimide-methyl-p-toluolsulp honate] cross-links L18 to 5S rRNA at pH 7.2 and L25 to 5S rRNA at pH 7.7. This pH-dependence of cross-linked proteins is a consequence of the difference in stability of the initial complex: the complex has all three proteins at pH 7.7 but L18 mainly at pH 7.2. It has been shown that L18 stimulates the chemical modification of U87 and U89 residues of 5S rRNA by carbodiimide. A model of L18-5S rRNA complex has been proposed.

8/3,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04377970 82235724
Endonucleases in yeast mitochondria: apurinic and manganese-stimulated deoxyribonuclease activities in the inner mitochondrial membrane of Saccharomyces cerevisiae.
Foury F
Eur J Biochem (GERMANY) May 17 1982, 124 (2) p253-9, ISSN 0014-2956 Journal Code: EMZ
Languages: ENGLISH
Document type: JOURNAL ARTICLE
An apurinic endonuclease activity has been characterized in yeast mitochondrial. It is dependent on Mg2+, stimulated by about 50% in the presence of 50 mM NaCl and inhibited at higher NaCl concentrations. It is located in the inner mitochondrial membrane and requires high concentrations of detergent (1.5-3% Triton X-100) to be extracted. The same treatment extracts several other endonuclease activities: the two Mg2+-dependent endonuclease activities cleaving double-stranded DNA at pH 7.5 and 5.4 respectively, the ethidium-bromide-stimulated endonuclease activity, the endonuclease activity cleaving single-stranded DNA at pH 7.15 [Jacquemin-Sablon et al. (1979) Biochemistry, 18, 119-127], and a manganese-stimulated deoxyribonuclease activity cleaving double-stranded DNA at pH 7.5 which has been discovered during the present work. Another endonuclease activity cleaving double-stranded DNA at pH 7.5 in the presence of Mg2+, slightly stimulated by low NaCl concentrations and inhibited by ethidium bromide is extracted from the membrane pellet remaining after the treatment with 1.5% Triton X-100 by a second treatment with 1.5% Triton X-100 plus 1 M KCl. The presence in the mitochondrial membrane of this apurinic endonuclease activity indicates that, like nuclear and prokaryotic DNA, yeast mitochondrial DNA is also subject to specialized repair systems.

8/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02920245 80056746
Accessibility of guanine at position 44 in the invariant sequence 5'CCG44AAC3' of Escherichia coli 5S RNA to reaction with kethoxal.
Larrinua I; Delihas N
Proc Natl Acad Sci U S A (UNITED STATES) Sep 1979, 76 (9) p4400-4,
ISSN 0027-8424 Journal Code: PV3
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The reaction of Escherichia coli ribosomes with beta-ethoxy-alpha-ketobutyraldehyde (kethoxal) in a buffer containing 50--100 mM Tris.HCl at pH 7.4, 50 mM NH4Cl, and 5 mM Mg(OAc)2 readily released the 5S RNA from the ribosomes. When liberated, the 5S RNA is in a conformation such that position 44 is selectively reactive, in addition to the normally reactive quanines at positions 41 and 13. Positions 41 and 13 have been previously shown to react in the 5S RNA in situ. The resulting new RNase T1 resistant oligonucleotides 5'CCG 44K AAUCAG51(3') and 5'ACCCCAUG 41KCCG 44KAACUCAG51(3') have been isolated and identified. These oligonucleotides have not been found in RNase T1 digests of 5S RNA that is not released from the ribosome. The guanine at position 44 is part of the invariant sequence 5'CCG44AAC3' which includes that portion of the molecule thought to interact with the invariant 5'GT psi C3' of tRNAs in the ribosomal A site. This invariant sequence of the 5S RNA may also form part of the binding site for protein L5.

8/3,AB/6 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08182552 BIOSIS NO.: 000094006325
THE INDIRECT IMMUNOFLUORESCENCE ASSAY IN THE DIAGNOSIS OF HUMAN ROTAVIRUS GASTROENTERITIS

AUTHOR: HARSI C M; CANDEIAS J A N
AUTHOR ADDRESS: INST. CIENCIAS BIOMEDICAS DA UNIV. DE SAO PAULO, DEP. DE MICROBIOL., AV. PROF. LINEU PRESTES, 1374, SAO PAULO, SP.

JOURNAL: REV MICROBIOL 22 (4). 1991. 282-287.
FULL JOURNAL NAME: Revista de Microbiologia
CODEN: RMBGB
RECORD TYPE: Abstract
LANGUAGE: PORTUGUESE

ABSTRACT: Rotavirus is the most frequently implicated etiological agent in infectious diarrhea in children. Several laboratory techniques were used to identify this virus in fecal material. This indirect immunofluorescence assay described by Briden et al was used in the work, with some modifications, to study the frequency of rotavirus in infecious diarrhea. The results were compared with those obtained with the enzyme immunoassay (EIARA) and the polyacrylamide gel electrophoresis (PAGE). The SA-11 strain of simian rotavirus was cultivated in MA-104 cells, in Eagle's MEM, without serum, with 10 .mu.g/ml of trypsin (1:250 Difco). The cultures with total cytophatic effect were clarifeid with Freon TF, DuPont. The virus was concentrated by ultracentrifugation at 100.00 g/15 min (Sorwall centrifuge OTD-75B with AH 627 rotor) and then purified in a 20-40% Cesium-Chloride gradient in Tris 0,05M, NaCl 0.15M buffer at 100.00 g/24h in a Beckmann L5-74 ultracentriguge with SW 65 rotor. This purified virus was used to prepare, in guinea-pigs, rotavirus antisera. Purified guinea-pig globulin was inoculated by subcutaneous

route in rabbits to obtain antiguinea pig .gamma.-globulin antiserum which was conjugated with fluorescein isothiocyanate (6). Fecal species were collected from 268 children, under one year of age, with acute diarrhea. Approximatedly 20% suspensions were made in Tris/HCl 0,01 M pH 7,4 buffer, containing 15 mM CaCl2, 1.00 U/ml penicillin and 1.00 .mu.g/ml of streptomycin. The suspensions were clarified by centrifugation at 12.350g/20min after homogenization with Freon TF, DuPont. The supernates were examined as described below, immediately or after storage at -20.degree. C. The immunofluorescence reaction was performed in polystyrene microtitration plates (NUNC), with 96 wells, coated with MA-104 cells monolayer. An 25 .mu.l amount of 20% fecal suspensions was inocualted in 2 wells, diluted at 1:4, and 25 .mu.l in other 2 wells diluted at 1:16. The wells were filled with 75 .mu.l of Eagle's MEM with 10.mu.g/ml of trypsin. The plates were centrifuged for 1 h at 1.200g in Beckmann TJ-6R centrifuge, with TH-4 rotor. The inoculum was poured out, the wells refilled with fresh medium, and the plates incubated at 37.degree. C for 18h. After incubation the plates were washed in PBS 0.01M pH 7,2,fixed with frozen methanol and allowed to dry. The infected monolayers were then treated with guinea-pig antirotavirus serum, diluted 1 in 40 (50 .mu.l/well), at 37.degree. C. After 60 min, plates were washed in PBS and stained for 60 min at 37.degree. C with the fluorescein-conjugated rabbit anti-guinea-pig serum, diluted 1 in 20 (50 .mu.l/well). After this period plates were washed in PBS, and allowed to dry. Readings of the fluorescence were performed in a Reichert-Jung, Microstar epifluorescent microscope. Samples with motor than 3 cells with cythoplasmic granular fluorescence were regarded as positive. Enzyme-immunoassays were performed by double antibody sandwich technique with the EIA-RA/FIOCRUZ kit by the technique described by Pereira et al. Electrophoresis was carried out by Laemlis technique with modifications described by Pereira et al. Slab gels were stained by silver impregnation. Rotavirus antigen could be detected in 40 out the 268 fecal samples (14,93%) by IF and PAGE, and in 46 (17,16%) by EIARA. A comparison between the three assays revealed a large percentage of agreement (72%). The results obtained were always using statistic kappa and the values obtained were between 0,72 and 0.76.

8/3,AB/7 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07520624 BIOSIS NO.: 000091083753
EVIDENCE THAT PROTEIN KINASE C MAY NOT BE INVOLVED IN THE INSULIN ACTION ON CYCLIC AMP PHOSPHODIESTERASE STUDIES WITH ELECTROPORATED RAT ADIPOCYTES THAT WERE HIGHLY RESPONSIVE TO INSULIN

AUTHOR: SHIBATA H; ROBINSON F W; BENZING C F; KONO T
AUTHOR ADDRESS: DEP. MOLECULAR PHYSIOL. BIOPHYSICS, SCH. MED., VANDERBILT UNIV., NASHVILLE, TENN. 37232-0615.

JOURNAL: ARCH BIOCHEM BIOPHYS 285 (1). 1991. 97-104.
FULL JOURNAL NAME: Archives of Biochemistry and Biophysics
CODEN: ABBIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Partially permeabilized rat adipocytes with a high responsiveness to insulin were prepared by electroporation and used to study the effect of 1-(5-isoquinolinylsulfonyl)-2-methylpiperazine (H-7) on insulin actions in adipocytes. H-7 is a well-documented inhibitor of several protein kinases, including protein kinase C; however, it does not rapidly enter adipocytes protected with the intact plasma membrane. The cells were suspended in Buffer X [4.74 nM NaCl, 118.0 mM KCl, 0.38 mM CaCl2, 1.00 mM EGTA, 1.19 mM Mg2SO4, 1.19 mM KH2PO4, 25.0 mM Hepes/K, 20 mg/ml bovine serum albumin, and 3 mM pyruvate/Na, pH 7.4] and

electroporated six times with a Gene-Pulser (from Bio-Rad) set at 25 .mu.F and 2 [redacted]m. In cells electroporated as [redacted]ove, insulin stimulated (a) membrane-bound, cAMP phosphodiesterase approximately 2.6-fold when the hormone concentration was 10 nM and (b) glucose transport activity approximately 4.15-fold when the hormone concentration was raised to 100 nM. H-7 strongly inhibited the actions of insulin on both glucose transport (apparent Ki = 0.3 mM) and cAMP phosphodiesterase (apparent Ki = 1.2 mM) in electroporated adipocytes. H-7 also inhibited lipolysis in adipocytes; the apparent Ki value for the reaction in intact cells was 0.45 mM, and that in electroporated cells was 0.075 mM. It is suggested that a certain protein kinase or kinases that are significantly sensitive to H-7 may be involved in the insulin-dependent stimulation of glucose transport and that of phosphodiesterase. However, protein kinase C (or Ca2+/phospholipid-dependent protein kinase) may not be involved, at least, in the hormonal action on phosphodiesterase since the apparent Ki value of H-7 for the reaction is too high.

8/3,AB/8 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07311383 BIOSIS NO.: 000090091276
STUDY OF THE 5S RIBOSOMAL RNA PROTEIN COMPLEX OF ESCHERICHIA-COLI BY MODIFYING IT WITH CARBODIIMIDE

AUTHOR: DONTSOVA O A; EFIMOV A V; KOPYLOV A M
AUTHOR ADDRESS: CHEM. FAC., M.V. LOMONOSOV MOSC. STATE UNIV., MOSCOW, USSR.

JOURNAL: BIOL NAUKI (MOSC) 0 (2). 1990. 22-30.
FULL JOURNAL NAME: Biologicheskie NAUKI (Moscow)
CODEN: BINKB
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

ABSTRACT: 5S rRNA-protein complex has been reconstituted from 5S rRNA and total protein of large (L) ribosomal subunit of Escherichia coli. The complex consists of 5S rRNA and 3 proteins only: L5, L18, L25. A water-soluble carbodiimide [N-cyclohexyl-N'-(2-morpholinoethyl)-carbodiimide-methyl-p-toluolsulphonate] cross-linkes L18 to 5S rRNA at pH 7,2 and L25 to 5S rRNA at pH 7,7. This pH-dependence of cross-linked proteins is a consequence of the difference in stability of the initial complex: the complex has all three proteins at pH 7,7 but L18 mainly at pH 7,2. It has been shown that L18 stimulates the chemical modification of U87 and U89 residues of 5S rRNA by carbodiimide. A model of L18-5S rRNA complex has been proposed.

8/3,AB/9 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05252647 BIOSIS NO.: 000082093272
ACETYLCHOLINESTERASE IN SEA-URCHIN SPHAERECHINUS-GRANULARIS SPERMATOZOA

AUTHOR: CARIELLO L; ROMANO G; NELSON L
AUTHOR ADDRESS: LAB. DI BIOCHIMICA, STAZIONE ZOOLOGICA, VILLA COMUNALE 80121, NAPOLI, ITALIA.

JOURNAL: GAMETE RES 14 (4). 1986. 323-332.
FULL JOURNAL NAME: Gamete Research
CODEN: GAMRD
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Flage[redacted] contain the bulk of spermato[redacted] acetylcholinesterase. Brief sonication of sea urchin sperm suspended in Tris-buffered (pH 8.0), Ca, Mg-free artificial sea water (F-ASW) containing 10 mM ethylene diaminetetracetic acid, (EDTA) doubled the specific activity over that of the intact spermatozoa. Lipids were removed from the solubilized supernatant of the tail membrane fraction by ether extraction. Hydrolysis of acetylthiocholine in the presence of dithiobisnitrobenzoic acid (DTNB) was monitored spectrophotometrically at 412 nm by the Ellman procedure. The enzyme was purified by affinity chromatography on a Sepharose cyanogen bromide gel to which the cholinesterase inhibitor trimethyl (para-aminophenyl) ammonium chloride was coupled. The enzyme was eluted from the column with a discontinuous NaCl gradient (0.1-0.5 M). The active fraction recovered at 0.35 M NaCl contained 0.007% of the initial total sperm cell protein with a 500-fold increase in specific activity. Twenty-four hr centrifugation on a 5-20% sucrose density gradient at 50,000 g in a Beckman L5-75 centrifuge yielded peaks at 14.7 S and 9.1 S. In the presence of 1% Triton X-100, three peaks appeared: 23.3 S, 13.7 S, and 9.1 S. These sedimentation coefficients resemble those of the electroplax acetylcholinesterase (AChE) forms A8 and A4. Eserine completely inhibited the activity of the purified enzyme, which exhibits a substrate optimum at 4 mM acetylcholine. The activity is depressed by 75% at 10 mM ACh and by 90% at 25 mM. The Km was 2.1 .times. 10-4 M. In the sperm cell the enzyme that terminates the action of intracellularly synthesized ACh may be involved in controlling ionophoric channels that regulate transmembrane transport of calcium.

8/3,AB/10 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

03504601 BIOSIS NO.: 000073007681
ANALYSES OF 40S RIBOSOMAL AND 60S RIBOSOMAL PROTEINS OF ARTEMIA-SALINA WITH 2 DIMENSIONAL OR 3 DIMENSIONAL ACRYLAMIDE GEL ELECTROPHORESIS AND COMPARISONS WITH RAT LIVER 40S PROTEINS AND 60S PROTEINS

AUTHOR: KENMOCHI N; TSURUGI K; OGATA K
AUTHOR ADDRESS: DEP. OF BIOCHEM., NIIGATA UNIV. SCH. OF MED., ASAHIMACHI-DORI, NIIGATA, NIIGATA 951.

JOURNAL: J BIOCHEM (TOKYO) 89 (4). 1981. 1293-1308.
FULL JOURNAL NAME: Journal of Biochemistry (Tokyo)
CODEN: JOBIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Basic proteins of 40 and 60S subunits of A. salina and rat liver were analyzed using 2 different systems of 2-dimensional acrylamide gel electrophoresis. In system I, the 1st dimension was run at pH 8.6 and the 2nd at pH 4.9, and in system II, the 1st was run at pH 8.6 and the 2nd in the presence of SDS [sodium dodecyl sulfate]. Three-dimensional electrophoresis was further used for the identification of individual ribosomal proteins. A. salina 40S proteins were separated into 27 proteins by 3-dimensional gel electrophoresis. Their 2-dimensional electrophoretogram in system I was somewhat different from that of liver 40S subunits, especially in the less basic region near the origin. Individual A. salina 40S proteins were designated according to their correspondence to their correspondence to 40S proteins of rat liver. The proteins S8 or S9 of both subunits overlapped between the 2 spp. Proteins corresponding to rat liver S3b, S5a and S5 proteins were not detected in A. salina 40S proteins. Forty-S proteins of A. salina and rat liver were further analyzed by 2-dimensional gel electrophoresis in system II. S7, S9 and S29 proteins overlapped between the 2 spp. Thus, S9

protein may have been almost completely conserved during evolution. Proteins (38) were identified in A. salina 60S proteins by 3-dimensional electrophoresis. The pattern was different from that of rat liver, especially in the basic region on 2-dimensional gels in systems I and II. Although the correspondence of individual proteins between the 2 spp. was very difficult to find, A. salina 60S proteins were designated by considering the mutual relationship to rat liver 60S proteins on the gel. L5, L31, L18 and L18a proteins of A. salina appeared to shift to more acidic regions as compared with corresponding 60S proteins of rat liver. The average MW of 40S proteins were 18,600 for A. salina (27 proteins) and 18,500 for rat liver (29 proteins). Those of 60S proteins were 21,600 for A. salina (38 proteins), 21,800 for rat liver (38 proteins). The average relative basicities of 40S proteins were similar in both species; the average of the A. salina 60S proteins was < that of rat liver. The protein moiety of 40S ribosomes has been conserved more than that of 60S ribosomes during animal evolution.

8/3,AB/11 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02655705 BIOSIS NO.: 000067043770
PARAMETERS FOR THE INTERACTION OF RIBOSOMAL PROTEINS L-5 L-18 AND L-25 WITH 5S RNA FROM ESCHERICHIA-COLI

AUTHOR: SPIERER P; BOGDANOV A A; ZIMMERMANN R A
AUTHOR ADDRESS: DEP. BIOCHEM., UNIV. MASS., AMHERST, MASS. 01003, USA.

JOURNAL: BIOCHEMISTRY 17 (25). 1978. 5394-5398.
FULL JOURNAL NAME: Biochemistry
CODEN: BICHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Association constants (Ka') for the binding of 50S ribosomal subunit proteins L5, L18 and L25 to the 5S rRNA of E. coli were determined by a membrane filter assay. Values for Ka' are 2.3 .times. 108 M-1 for the L18-5S RNA complex, 1.5 .times. 107 M-1 for the L25-5S RNA complex, and 2.3 .times. 106 M-1 for the L5-5S RNA complex at 25.degree. C in TMK buffer (50 mM Tris-HCl (pH 7.6)-20 mM MgCl2-300 mM KCl). Although the affinity of L5 increases by about 1 order of magnitude in the presence of L18, estimation of Ka' was not feasible in the ternary complex. Standard thermodynamic quantities for the individual protein-5S RNA interactions were calculated from the variation of Ka' with temperature. Enthalpy and entropy changes both contribute to the free energy of binding in all 3 cases. Since the enthalpic terms are small, it is unlikely that the associations lead to major alterations in the structure of the ribosomal components. Circular dichroism [CD] measurements confirm that the 5S RNA undergoes no detectable change in secondary structure as a result of association with L5 or L25. Formation of the L18-5S RNA complex, by contrast, is accompanied by a significant increase in the CD at 268 nm, suggesting that the protein induces a shift in the configuration of one of the double-stranded regions of the RNA molecule. This observation may help to explain the strong cooperative influence of L18 upon the binding of L5 to the 5S RNA.

8/3,AB/12 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02471887 BIOSIS NO.: 000066054432
STOICHIOMETRY COOPERATIVITY AND STABILITY OF INTERACTIONS BETWEEN 5S RNA

AND PROTEINS L5 L-18 AND L-25 FROM THE 50S RIBOSOMAL SUBUNIT OF ESCHERICHIA-C[illegible]

AUTHOR: SPIERER P; ZIMMERMANN R A
AUTHOR ADDRESS: DEP. BIOCHEM., UNIV. MASS., AMHERST, MASS. 01003, USA.

JOURNAL: BIOCHEMISTRY 17 (13). 1978 2474-2479.
FULL JOURNAL NAME: Biochemistry
CODEN: BICHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Interactions of 5S RNA from E. coli with 50S ribosomal subunit proteins L5, L18 and L25 were evaluated by a number of criteria. The dependence of complex formation on protein and RNA concentration in TMK buffer (50 mM Tris-HCl (pH 7.6)-20 mM MgCl2-300 mM KCl) indicated that the 3 proteins differ substantially in their affinity for the nucleic acid. Measurement of the stoichiometry of association in the presence of excess protein revealed that molar protein:RNA binding ratios for L5, L18 and L25 at saturation were 0.6:1, 1.1:1 and 0.7:1, respectively. The RNA molecule therefore contains no more than 1 specific site of attachment for each of the proteins. Solution conditions were varied to assess the effects of pH, Mg2+ concentration and K+ concentration on the stability of the interactions. Optimal binding was observed for the L5-5S RNA complex at pH 6.5-9, [Mg2+] of 10-20 mM and [K+] of 300 to 400 mM; for the L18-5S RNA complex at pH 7 .5-9, [Mg2+] of 10-20 mM and [K+] of 100-200 mM; and for the L25-5S RNA complex at pH 7.5-9, [Mg2+] of 0.3-20 mM and [K+] of 200-300 mM. In a separate series of experiments, the association of L5 and TMK buffer was cooperatively stimulated by L18 at component concentrations roughly tenfold less than were required for the association of L5 alone. The mutual influence of these 2 proteins upon one another was also clearly manifested in assays involving variation of pH and ionic environment. The pattern of cooperativity showed that the binding sites for L5 and L18 in the 5S RNA are functionally related to each other, but distinct from that for protein

drug resistance and occurrence of the often severe retinoic acid syndrome. Useful strategies have been described to manage these effects but current and future efforts must be directed at elucidating the mechanisms involved and determining the optimum therapeutic management. In summary, results to date indicate that the combination of tretinoin and intensive chemotherapy is more effective than chemotherapy alone and appears to improve the prognosis of newly diagnosed patients with acute promyelocytic leukaemia. Further information on the relative efficacy of various induction and post-remission strategies in subsets of patients will help determine optimum use of this promising agent in the management of acute promyelocytic leukaemia.

4/3,AB/13 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08382460 95363500
Biology and therapy of pediatric rhabdomyosarcoma [see comments]
Pappo AS; Shapiro DN; Crist WM; Maurer HM
Department of Hematology/Oncology, St Jude Children's Research Hospital, Memphis, TN 38101, USA.
J Clin Oncol (UNITED STATES) Aug 1995, 13 (8) p2123-39, ISSN 0732-183X Journal Code: JCO
Contract/Grant No.: CA 23099, CA, NCI; P30 CA 21765, CA, NCI
Comment in J Clin Oncol 1996 Jan;14(1):323
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL
PURPOSE: To review key developments in biology and therapy of rhabdomyosarcoma (RMS) since the early 1970s. PATIENTS AND METHODS: The literature regarding biology, therapy, and late effects of therapy through March 1995 was reviewed. RESULTS: The two major histiotypes, embryonal and alveolar, are characterized by specific genetic abnormalities that provide clues to mechanisms of tumor induction. Alveolar tumors, for example, often possess a chromosomal translocation [t(2;13)(q35;q14)] that fuses the PAX3 gene in band 2q35 with the FKHR gene in band 13q14, creating a novel chimeric protein that could inappropriately activate normal targets of the PAX3 gene product, thereby contributing to tumorigenesis. Recognition of prognostically important patient groups primarily identified by tumor extent, site, and histology, and development of effective risk-based multimodal therapy in randomized trials, have increased long-term survival in RMS from 25% in 1970 to more than 70% in current studies. The most significant recent gain in therapeutic results was realized in patients with gross residual tumor after biopsy. CONCLUSION: Contemporary risk-based therapy cures more than two thirds of children with RMS while minimizing acute and late effects. Increased dose-intensity of known effective agents with hematopoietic growth factor support, new agents, and hyperfractionated irradiation are being evaluated in hopes of further improving therapy. Recent discovery of novel genetic features in this tumor should lead to better methods of diagnosis and risk assessment, and ultimately to identification of molecular targets for specific treatment.

4/3,AB/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08325208 95283224
Immunohistology, cytogenetics, and molecular studies of small round cell tumors of childhood. A review.
Winters JL; Geil JD; O'Connor WN
Department of Pathology and Laboratory Medicine, College of Medicine, University of Kentucky, Lexington 40536, USA.
Ann Clin Lab Sci (UNITED STATES) Jan-Feb 1995, 25 (1) p66-78, ISSN

activated by fusion of its 3' half to different genes: characterization of the set gene.

von Lindern M; van Baal S; Wiegant J; Raap A; Hagemeijer A; Grosveld G

Department of Cell Biology and Genetics, Erasmus University, Rotterdam, The Netherlands.

Mol Cell Biol (UNITED STATES) Aug 1992, 12 (8) p3346-55, ISSN 0270-7306 Journal Code: NGY

QH 506.M6

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The **translocation** (6;9)(p23;q34) in acute nonlymphocytic leukemia results in the formation of a highly consistent dek-can fusion gene. **Translocation** breakpoints invariably occur in single introns of dek and can, which were named icb-6 and icb-9, respectively. In a case of acute undifferentiated leukemia, a breakpoint was detected in icb-9 of can, whereas no breakpoint could be detected in dek. Genomic and cDNA cloning showed that instead of dek, a different gene was fused to can, which was named set. set encodes transcripts of 2.0 and 2.7 kb that result from the use of alternative polyadenylation sites. Both transcripts contain the open reading frame for a putative SET protein with a predicted molecular mass of 32 kDa. The set-can fusion gene is transcribed into a 5-kb transcript that contains a single open reading frame predicting a 155-kDa chimeric SET-CAN protein. The SET sequence shows homology with the yeast nucleosome assembly protein NAP-I. The only common sequence motif of SET and DEK proteins is an acidic region. SET has a long acidic tail, of which a large part is present in the predicted SET-CAN fusion protein. The set gene is located on **chromosome** 9q34, centromeric of c-abl. Since a dek-can fusion gene is present in t(6;9) acute myeloid leukemia and a set-can fusion gene was found in a case of acute undifferentiated leukemia, we assume that can may function as an oncogene activated by fusion of its 3' part to dek, set, or perhaps other genes.

2/3,AB/12 (Item 12 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

07004232 92073906

Characterization of a zinc finger gene disrupted by the t(15;17) in acute promyelocytic leukemia.

Goddard AD; Borrow J; Freemont PS; Solomon E

Somatic Cell Genetics Laboratory, Imperial Cancer Research Fund, London, United Kingdom.

Science (UNITED STATES) Nov 29 1991, 254 (5036) p1371-4, ISSN 0036-8075 Journal Code: UJ7

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The **translocation** t(15;17) associated with acute promyelocytic leukemia results in the fusion of the retinoic acid receptor alpha (RARA) gene to the PML gene. Characterization of PML revealed that it is a putative zinc finger protein and potential transcription factor that is commonly expressed, with at least three major transcription products. PML breakpoints cluster in two regions on either side of an alternatively spliced exon. Although leukemic cells with **translocations** characteristically express only one fusion product, both PML/RARA (on the 15q+ derivative **chromosome**) and RARA/PML (on the 17q- derivative) are transcribed.

2/3,AB/13 (Item 13 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

06978765 90214615

bcr-abl, the hallmark of chronic myeloid leukaemia in man, induces multiple haemopoietic neoplasms in mice.

```
=> s chromosom? and translocat?

         11003 CHROMOSOM?
          3622 TRANSLOCAT?
L1        1648 CHROMOSOM? AND TRANSLOCAT?

=> s l1 and t(1;19)

MISSING OPERATOR 'AND T(1'

COMMAND STACK INTERRUPTED.  ENTER "DISPLAY HISTORY"
TO SEE WHICH COMMANDS WERE EXECUTED.

=> s l1 and t(w)1(w)19

        568462 T
       2484221 1
       1161286 19
            23 T(W)1(W)19
L2           2 L1 AND T(W)1(W)19

=> d ti 1-2


US PAT NO:      5,858,682 [IMAGE AVAILABLE]          L2: 1 of 2
TITLE:          E2A/pbx1 fusion protein specific monoclonal antibodies

US PAT NO:      5,783,387 [IMAGE AVAILABLE]          L2: 2 of 2
TITLE:          Method for identifying and quantifying nucleic acid
                  sequence aberrations

=> s l1 and t(w)2(w)5

        568462 T
       2481447 2
       2356415 5
            86 T(W)2(W)5
L3           0 L1 AND T(W)2(W)5

=> s l1 and t(w)2(w)13

        568462 T
       2481447 2
       1634604 13
            14 T(W)2(W)13
L4           0 L1 AND T(W)2(W)13

=> s l1 and 4(w)11

       2425531 4
       1806791 11
          5933 4(W)11
L5           37 L1 AND 4(W)11

=> d 1-37 ti


US PAT NO:      5,936,147 [IMAGE AVAILABLE]          L5: 1 of 37
```

5,567,586
5,633,135 ✓✓
5,487,970 ✓✓✓✓✓
5,449,604
5,633,136 ✓
5,648,212
5,849,996
5,491,283
5,~~827~~,066,792 ✓
5,026,837
4,857,466
4,681,840
5,677,130
5,543,296
4,963,633
5,888,779
5,824,518
5,480,784
5,399,491
5,482,834

TITLE: Hybrid maize plant and seed 33H67

US PAT NO: 5,889,189 [IMAGE AVAILABLE] L5: 2 of 37
TITLE: Process for protein production in plants

US PAT NO: 5,888,789 [IMAGE AVAILABLE] L5: 3 of 37
TITLE: Process for protein production in plants

US PAT NO: 5,877,161 [IMAGE AVAILABLE] L5: 4 of 37
TITLE: Cyclin D1 negative regulatory activity

US PAT NO: 5,869,337 [IMAGE AVAILABLE] L5: 5 of 37
TITLE: Regulated transcription of targeted genes and other biological events

US PAT NO: 5,850,009 [IMAGE AVAILABLE] L5: 6 of 37
TITLE: Inbred maize line PH0HC

US PAT NO: 5,844,117 [IMAGE AVAILABLE] L5: 7 of 37
TITLE: Inbred maize line PHOGP

US PAT NO: 5,844,116 [IMAGE AVAILABLE] L5: 8 of 37
TITLE: Inbred maize line PH1W2

US PAT NO: 5,837,500 [IMAGE AVAILABLE] L5: 9 of 37
TITLE: Directed evolution of novel binding proteins

US PAT NO: 5,817,918 [IMAGE AVAILABLE] L5: 10 of 37
TITLE: Hybrid maize plant & seed (38R21)

US PAT NO: 5,811,638 [IMAGE AVAILABLE] L5: 11 of 37
TITLE: Hybrid maize plant and seed (3743E)

US PAT NO: 5,792,929 [IMAGE AVAILABLE] L5: 12 of 37
TITLE: Plants with modified flowers

US PAT NO: 5,773,684 [IMAGE AVAILABLE] L5: 13 of 37
TITLE: Hybrid maize plant and seed (39B42)

US PAT NO: 5,767,374 [IMAGE AVAILABLE] L5: 14 of 37
TITLE: Plants with modified flowers seeds or embryos

US PAT NO: 5,767,340 [IMAGE AVAILABLE] L5: 15 of 37
TITLE: Inbred maize line PHBR2

US PAT NO: 5,763,743 [IMAGE AVAILABLE] L5: 16 of 37
TITLE: Inbred maize line PH63A

US PAT NO: 5,731,492 [IMAGE AVAILABLE] L5: 17 of 37
TITLE: Inbred maize line PH19A

US PAT NO: 5,723,763 [IMAGE AVAILABLE] L5: 18 of 37
TITLE: Plants with modified flowers

US PAT NO: 5,723,722 [IMAGE AVAILABLE] L5: 19 of 37
TITLE: Inbred maize line PHND1

US PAT NO: 5,693,506 [IMAGE AVAILABLE] L5: 20 of 37
TITLE: Process for protein production in plants

US PAT NO: 5,689,041 [IMAGE AVAILABLE] L5: 21 of 37
TITLE: Plants modified with barstar for fertility restoration

US PAT NO: 5,689,034 [IMAGE AVAILABLE] L5: 22 of 37
TITLE: Inbred maize line PH24E

US PAT NO: [redacted]52,354 [IMAGE AVAILABLE] L5: 23 of 37
TITLE: Stamen-selective promoters

US PAT NO: 5,635,351 [IMAGE AVAILABLE] L5: 24 of 37
TITLE: Genetic gain and loss in gliomas

US PAT NO: 5,633,441 [IMAGE AVAILABLE] L5: 25 of 37
TITLE: Plants with genetic female sterility

US PAT NO: 5,633,135 [IMAGE AVAILABLE] L5: 26 of 37
TITLE: Chimeric nucleic acids and proteins resulting from ALL-1 region **chromosome** abnormalities

US PAT NO: 5,571,698 [IMAGE AVAILABLE] L5: 27 of 37
TITLE: Directed evolution of novel binding proteins

US PAT NO: 5,569,819 [IMAGE AVAILABLE] L5: 28 of 37
TITLE: Inbred maize line PHPP8

US PAT NO: 5,563,325 [IMAGE AVAILABLE] L5: 29 of 37
TITLE: Inbred maize line PHBE2

US PAT NO: 5,563,321 [IMAGE AVAILABLE] L5: 30 of 37
TITLE: Inbred maize line PHGF5

US PAT NO: 5,563,320 [IMAGE AVAILABLE] L5: 31 of 37
TITLE: Inbred maize line PH54B

US PAT NO: 5,552,530 [IMAGE AVAILABLE] L5: 32 of 37
TITLE: Antibodies that specifically bind to and inhibit human synovial phospholipase A.sub.2 type A

US PAT NO: 5,487,970 [IMAGE AVAILABLE] L5: 33 of 37
TITLE: Compositions and methods for detecting gene rearrangements and **translocations**

US PAT NO: 5,449,604 [IMAGE AVAILABLE] L5: 34 of 37
TITLE: **Chromosome** 14 and familial Alzheimers disease genetic markers and assays

US PAT NO: 5,403,484 [IMAGE AVAILABLE] L5: 35 of 37
TITLE: Viruses expressing chimeric binding proteins

US PAT NO: 5,223,409 [IMAGE AVAILABLE] L5: 36 of 37
TITLE: Directed evolution of novel binding proteins

US PAT NO: 5,019,508 [IMAGE AVAILABLE] L5: 37 of 37
TITLE: Synovial phospholipases

```
=> s l1 and human

        188640 HUMAN
         47752 HUMANS
        202886 HUMAN
                 (HUMAN OR HUMANS)
L6        1456 L1 AND HUMAN

=> s l6 and detect? and amplif?

        560076 DETECT?
        262639 AMPLIF?
L7        1042 L6 AND DETECT? AND AMPLIF?

=> s l7 and 6(w)9
```

```
      2250463 6
      1827563 9
        12329 6(W)9
L8          28 L7 AND 6(W)9

=> d ti 1-27
```

US PAT NO: 5,912,147 [IMAGE AVAILABLE] L8: 1 of 28
TITLE: Rapid means of quantitating genomic instability

US PAT NO: 5,874,304 [IMAGE AVAILABLE] L8: 2 of 28
TITLE: Humanized green fluorescent protein genes and methods

US PAT NO: 5,872,230 [IMAGE AVAILABLE] L8: 3 of 28
TITLE: Compositions and methods for regulation of steroidogenesis

US PAT NO: 5,843,775 [IMAGE AVAILABLE] L8: 4 of 28
TITLE: **Human** dorsal tissue affecting factor (noggin) and nucleic acids encoding same

US PAT NO: 5,840,489 [IMAGE AVAILABLE] L8: 5 of 28
TITLE: Diagnosis and treatment of supravalvular aortic stenosis and Williams syndrome

US PAT NO: 5,834,247 [IMAGE AVAILABLE] L8: 6 of 28
TITLE: Modified proteins comprising controllable intervening protein sequences or their elements methods of producing same and methods for purification of a target protein comprised by a modified protein

US PAT NO: 5,831,058 [IMAGE AVAILABLE] L8: 7 of 28
TITLE: **Human** GDP dissociation stimulating protein gene

US PAT NO: 5,824,770 [IMAGE AVAILABLE] L8: 8 of 28
TITLE: Ikaros polypeptides

US PAT NO: 5,824,507 [IMAGE AVAILABLE] L8: 9 of 28
TITLE: Hepatitis G virus and molecular cloning thereof

US PAT NO: 5,807,836 [IMAGE AVAILABLE] L8: 10 of 28
TITLE: Interferon regulatory factors 1 and 2 in the diagnosis of tumorigenicity

US PAT NO: 5,804,374 [IMAGE AVAILABLE] L8: 11 of 28
TITLE: Nuclear factors associates with transcriptional regulation

US PAT NO: 5,773,215 [IMAGE AVAILABLE] L8: 12 of 28
TITLE: Tumor marker protein for cancer risk assessment

US PAT NO: 5,770,396 [IMAGE AVAILABLE] L8: 13 of 28
TITLE: Isolation characterization, and use of the **human** beta subunit of the high affinity receptor for immunoglobulin E

US PAT NO: 5,723,300 [IMAGE AVAILABLE] L8: 14 of 28
TITLE: Nuclear localized transcription factor kinase and diagnostic assays related thereto

US PAT NO: 5,677,172 [IMAGE AVAILABLE] L8: 15 of 28
TITLE: Method for production of proteins in yeast

US PAT NO: 5,652,095 [IMAGE AVAILABLE] L8: 16 of 28
TITLE: Interferon regulatory factors 1 and 2 in the diagnosis of

tumorigenicity

US PAT NO: 5,650,282 [IMAGE AVAILABLE] L8: 17 of 28
TITLE: Diagnosis of Williams syndrome

US PAT NO: 5,633,136 [IMAGE AVAILABLE] L8: 18 of 28
TITLE: ALL-1 polynucleotides for leukemia **detection** and treatment

US PAT NO: 5,633,135 [IMAGE AVAILABLE] L8: 19 of 28
TITLE: Chimeric nucleic acids and proteins resulting from ALL-1 region **chromosome** abnormalities

US PAT NO: 5,610,011 [IMAGE AVAILABLE] L8: 20 of 28
TITLE: Virulence-encoding DNA sequences of Strepococcus suis and related products and methods

US PAT NO: 5,578,493 [IMAGE AVAILABLE] L8: 21 of 28
TITLE: Wilson's disease gene

US PAT NO: 5,567,586 [IMAGE AVAILABLE] L8: 22 of 28
TITLE: Methods of indentifying solid tumors with **chromosome** abnormalities in the ALL-1 region

US PAT NO: 5,539,096 [IMAGE AVAILABLE] L8: 23 of 28
TITLE: Genes differentially expressed in metastatic and non-metastatic rat rhabdomyosarcoma cell lines

US PAT NO: 5,536,636 [IMAGE AVAILABLE] L8: 24 of 28
TITLE: Methods for identifying a tyrosine phosphatase abnormality associated with neoplastic disease

US PAT NO: 5,487,970 [IMAGE AVAILABLE] L8: 25 of 28
TITLE: Compositions and methods for **detecting** gene rearrangements and **translocations**

US PAT NO: 5,273,905 [IMAGE AVAILABLE] L8: 26 of 28
TITLE: Processing of slide mounted material

US PAT NO: 5,198,346 [IMAGE AVAILABLE] L8: 27 of 28
TITLE: Generation and selection of novel DNA-binding proteins and polypeptides

=> s l7 and 8(w)21

```
      1989504 8
      1216070 21
         1415 8(W)21
L9          5 L7 AND 8(W)21
```

=> d ti 1-5

US PAT NO: 5,928,926 [IMAGE AVAILABLE] L9: 1 of 5
TITLE: Isolation and cloning of the **human** ARSA-I gene and uses thereof

US PAT NO: 5,925,530 [IMAGE AVAILABLE] L9: 2 of 5
TITLE: Simple method for the **detection** of minimal residual disease to predict relapse of acute lymphoblastic leukaemia

US PAT NO: 5,849,996 [IMAGE AVAILABLE] L9: 3 of 5
TITLE: BCR/ABL transgenic animals as models for Philadelphia **chromosome** positive chronic myelogenous and acute

lymphoblastic leukemia

L9: 4 of 5

US PAT NO: 5,547,838 [IMAGE AVAILABLE]
TITLE: Method for the rapid and ultra-sensitive **detection** of leukemic cells

L9: 5 of 5

US PAT NO: 5,491,283 [IMAGE AVAILABLE]
TITLE: BRC/ABL transgenic animals as models for Philadelphia **chromosome** positive chronic myelogenous and acute lymphoblastic leukemia

=> s l7 and 9(w)11

```
       1827563 9
       1806791 11
         12539 9(W)11
L10         28 L7 AND 9(W)11
```

=> d ti 1-28

L10: 1 of 28

US PAT NO: 5,928,900 [IMAGE AVAILABLE]
TITLE: Bacterial exported proteins and acellular vaccines based thereon

L10: 2 of 28

US PAT NO: 5,869,337 [IMAGE AVAILABLE]
TITLE: Regulated transcription of targeted genes and other biological events

L10: 3 of 28

US PAT NO: 5,856,097 [IMAGE AVAILABLE]
TITLE: Comparative genomic hybridization (CGH)

L10: 4 of 28

US PAT NO: 5,846,763 [IMAGE AVAILABLE]
TITLE: DNA encoding tumor necrosis factor stimulated gene 6 (TSG-6)

L10: 5 of 28

US PAT NO: 5,837,500 [IMAGE AVAILABLE]
TITLE: Directed evolution of novel binding proteins

L10: 6 of 28

US PAT NO: 5,834,266 [IMAGE AVAILABLE]
TITLE: Regulated apoptosis

L10: 7 of 28

US PAT NO: 5,830,462 [IMAGE AVAILABLE]
TITLE: Regulated transcription of targeted genes and other biological events

L10: 8 of 28

US PAT NO: 5,824,770 [IMAGE AVAILABLE]
TITLE: Ikaros polypeptides

L10: 9 of 28

US PAT NO: 5,807,836 [IMAGE AVAILABLE]
TITLE: Interferon regulatory factors 1 and 2 in the diagnosis of tumorigenicity

L10: 10 of 28

US PAT NO: 5,770,396 [IMAGE AVAILABLE]
TITLE: Isolation characterization, and use of the **human** beta subunit of the high affinity receptor for immunoglobulin E

L10: 11 of 28

US PAT NO: 5,763,584 [IMAGE AVAILABLE]
TITLE: Receptor activation with hepatocyte growth factor agonists

L10: 12 of 28

US PAT NO: 5,721,098 [IMAGE AVAILABLE]
TITLE: Comparative genomic hybridization

L10: 13 of 28

US PAT NO: 5,684,136 [IMAGE AVAILABLE]

TITLE: [redacted]meric hepatocyte growth factor [redacted]GF) ligand variants

US PAT NO: 5,665,549 [IMAGE AVAILABLE] L10: 14 of 28
TITLE: Comparative genomic hybridization (CGH)

US PAT NO: 5,652,095 [IMAGE AVAILABLE] L10: 15 of 28
TITLE: Interferon regulatory factors 1 and 2 in the diagnosis of tumorigenicity

US PAT NO: 5,633,135 [IMAGE AVAILABLE] L10: 16 of 28
TITLE: Chimeric nucleic acids and proteins resulting from ALL-1 region **chromosome** abnormalities

US PAT NO: 5,599,920 [IMAGE AVAILABLE] L10: 17 of 28
TITLE: Peripheral myelin protein coding sequence and method

US PAT NO: 5,571,706 [IMAGE AVAILABLE] L10: 18 of 28
TITLE: Plant virus resistance gene and methods

US PAT NO: 5,571,698 [IMAGE AVAILABLE] L10: 19 of 28
TITLE: Directed evolution of novel binding proteins

US PAT NO: 5,536,636 [IMAGE AVAILABLE] L10: 20 of 28
TITLE: Methods for identifying a tyrosine phosphatase abnormality associated with neoplastic disease

US PAT NO: 5,487,970 [IMAGE AVAILABLE] L10: 21 of 28
TITLE: Compositions and methods for **detecting** gene rearrangements and **translocations**

US PAT NO: 5,403,484 [IMAGE AVAILABLE] L10: 22 of 28
TITLE: Viruses expressing chimeric binding proteins

US PAT NO: 5,395,767 [IMAGE AVAILABLE] L10: 23 of 28
TITLE: Gene for ataxia-telangiectasia complementation group D (ATDC)

US PAT NO: 5,223,409 [IMAGE AVAILABLE] L10: 24 of 28
TITLE: Directed evolution of novel binding proteins

US PAT NO: 5,066,792 [IMAGE AVAILABLE] L10: 25 of 28
TITLE: Gene probe for **detection** of specific **human** leukemias

US PAT NO: 5,026,837 [IMAGE AVAILABLE] L10: 26 of 28
TITLE: DNA probe which reveals a hypervariable region on **human chromosome** 16

US PAT NO: 4,857,466 [IMAGE AVAILABLE] L10: 27 of 28
TITLE: Probe for **detection** of specific **human** leukemias

US PAT NO: 4,681,840 [IMAGE AVAILABLE] L10: 28 of 28
TITLE: Deoxyribonucleic acid molecules useful as probes for **detecting** oncogenes incorporated into **chromosomal** DNA

```
=> s l7 and 11(w)14

       1806791 11
       1881885 14
          6131 11(W)14
L11          18 L7 AND 11(W)14

=> d ti 1-18
```

US PAT NO: 5,874,563 [IMAGE AVAILABLE] L11: 1 of 18
TITLE: Hepatitis G virus and molecular cloning thereof

US PAT NO: 5,872,230 [IMAGE AVAILABLE] L11: 2 of 18
TITLE: Compositions and methods for regulation of steroidogenesis

US PAT NO: 5,869,045 [IMAGE AVAILABLE] L11: 3 of 18
TITLE: Antibody conjugates reactive with **human** carcinomas

US PAT NO: 5,856,134 [IMAGE AVAILABLE] L11: 4 of 18
TITLE: Hepatitis G virus and molecular cloning thereof

US PAT NO: 5,849,532 [IMAGE AVAILABLE] L11: 5 of 18
TITLE: Hepatitis G virus and molecular cloning thereof

US PAT NO: 5,834,266 [IMAGE AVAILABLE] L11: 6 of 18
TITLE: Regulated apoptosis

US PAT NO: 5,831,058 [IMAGE AVAILABLE] L11: 7 of 18
TITLE: **Human** GDP dissociation stimulating protein gene

US PAT NO: 5,824,507 [IMAGE AVAILABLE] L11: 8 of 18
TITLE: Hepatitis G virus and molecular cloning thereof

US PAT NO: 5,807,836 [IMAGE AVAILABLE] L11: 9 of 18
TITLE: Interferon regulatory factors 1 and 2 in the diagnosis of tumorigenicity

US PAT NO: 5,766,840 [IMAGE AVAILABLE] L11: 10 of 18
TITLE: Hepatitis G virus and molecular cloning thereof

US PAT NO: 5,677,130 [IMAGE AVAILABLE] L11: 11 of 18
TITLE: BCL-1 locus nucleic acid probes and assay methods

US PAT NO: 5,652,095 [IMAGE AVAILABLE] L11: 12 of 18
TITLE: Interferon regulatory factors 1 and 2 in the diagnosis of tumorigenicity

US PAT NO: 5,618,715 [IMAGE AVAILABLE] L11: 13 of 18
TITLE: Oncostatin M and novel compositions having anti-neoplastic activity

US PAT NO: 5,487,970 [IMAGE AVAILABLE] L11: 14 of 18
TITLE: Compositions and methods for **detecting** gene rearrangements and **translocations**

US PAT NO: 5,451,506 [IMAGE AVAILABLE] L11: 15 of 18
TITLE: Oncostatin M and novel compositions having anti-neoplastic activity

US PAT NO: 5,428,012 [IMAGE AVAILABLE] L11: 16 of 18
TITLE: Oncostatin M and novel compositions having anti-neoplastic activity

US PAT NO: 5,395,767 [IMAGE AVAILABLE] L11: 17 of 18
TITLE: Gene for ataxia-telangiectasia complementation group D (ATDC)

US PAT NO: 5,196,333 [IMAGE AVAILABLE] L11: 18 of 18
TITLE: DNA sequences involved in neuronal degeneration, multicellular organisms containing same and uses thereof

=> s l7 and 11(w)19

```
      1806791
      1161286 19
         1763 11(W)19
L12         7 L7 AND 11(W)19

=> d ti 1-7


US PAT NO:      5,837,500 [IMAGE AVAILABLE]          L12: 1 of 7
TITLE:          Directed evolution of novel binding proteins

US PAT NO:      5,571,698 [IMAGE AVAILABLE]          L12: 2 of 7
TITLE:          Directed evolution of novel binding proteins

US PAT NO:      5,519,003 [IMAGE AVAILABLE]          L12: 3 of 7
TITLE:          WD-40-derived peptides and uses thereof

US PAT NO:      5,487,970 [IMAGE AVAILABLE]          L12: 4 of 7
TITLE:          Compositions and methods for detecting gene
                  rearrangements and translocations

US PAT NO:      5,403,484 [IMAGE AVAILABLE]          L12: 5 of 7
TITLE:          Viruses expressing chimeric binding proteins

US PAT NO:      5,273,905 [IMAGE AVAILABLE]          L12: 6 of 7
TITLE:          Processing of slide mounted material

US PAT NO:      5,223,409 [IMAGE AVAILABLE]          L12: 7 of 7
TITLE:          Directed evolution of novel binding proteins

=> s l7 and 11 (w)22

      1806791 11
      1607555 22
         1697 11 (W)22
L13         4 L7 AND 11 (W)22

=> d ti 1-4


US PAT NO:      5,935,783 [IMAGE AVAILABLE]          L13: 1 of 4
TITLE:          Genes mapping in the digeorge and velocardiofacial
                  syndrome minimal critical region

US PAT NO:      5,869,045 [IMAGE AVAILABLE]          L13: 2 of 4
TITLE:          Antibody conjugates reactive with human carcinomas

US PAT NO:      5,487,970 [IMAGE AVAILABLE]          L13: 3 of 4
TITLE:          Compositions and methods for detecting gene
                  rearrangements and translocations

US PAT NO:      5,066,792 [IMAGE AVAILABLE]          L13: 4 of 4
TITLE:          Gene probe for detection of specific human
                  leukemias

=> s l7 and 12(w)21

      2051705 12
      1216070 21
         1943 12(W)21
L14         8 L7 AND 12(W)21

=> d ti 1-8
```

US PAT NO: [redacted]
TITLE: Genes mapping in the digeorge and velocardiofacial syndrome minimal critical region

US PAT NO: 5,910,574 [IMAGE AVAILABLE] L14: 2 of 8
TITLE: **Human** trk receptors and neurotrophic factor inhibitors

US PAT NO: 5,766,888 [IMAGE AVAILABLE] L14: 3 of 8
TITLE: **Detection** of carcinoma metastases by nucleic acid **amplification**

US PAT NO: 5,545,553 [IMAGE AVAILABLE] L14: 4 of 8
TITLE: Glycosyltransferases for biosynthesis of oligosaccharides, and genes encoding them

US PAT NO: 5,543,296 [IMAGE AVAILABLE] L14: 5 of 8
TITLE: **Detection** of carcinoma metastases by nucleic acid **amplification**

US PAT NO: 5,411,859 [IMAGE AVAILABLE] L14: 6 of 8
TITLE: Genetic identification employing DNA probes of variable number tandem repeat loci

US PAT NO: 5,273,905 [IMAGE AVAILABLE] L14: 7 of 8
TITLE: Processing of slide mounted material

US PAT NO: 4,963,663 [IMAGE AVAILABLE] L14: 8 of 8
TITLE: Genetic identification employing DNA probes of variable number tandem repeat loci

=> s l7 and 14(w)18

```
       1881885 14
       1659388 18
          6343 14(W)18
L15          21 L7 AND 14(W)18
```

=> d ti 1-21

US PAT NO: 5,888,779 [IMAGE AVAILABLE] L15: 1 of 21
TITLE: Kits for nucleic acid sequence **amplification** methods

US PAT NO: 5,885,831 [IMAGE AVAILABLE] L15: 2 of 21
TITLE: Nuclear localization factor associated with circadian rhythms

US PAT NO: 5,869,640 [IMAGE AVAILABLE] L15: 3 of 21
TITLE: Nucleic acids encoding D-type cyclins and hybridization probes

US PAT NO: 5,849,535 [IMAGE AVAILABLE] L15: 4 of 21
TITLE: **Human** growth hormone variants

US PAT NO: 5,837,500 [IMAGE AVAILABLE] L15: 5 of 21
TITLE: Directed evolution of novel binding proteins

US PAT NO: 5,830,644 [IMAGE AVAILABLE] L15: 6 of 21
TITLE: Method for screening for agents which increase telomerase activity in a cell

US PAT NO: 5,824,518 [IMAGE AVAILABLE] L15: 7 of 21
TITLE: Nucleic acid sequence **amplification** methods

US PAT NO: 5,795,713 [IMAGE AVAILABLE] L15: 8 of 21

TITLE: [redacted]ods for identifying inducers [redacted] inhibitors of programmed cell death

US PAT NO: 5,753,231 [IMAGE AVAILABLE] L15: 9 of 21
TITLE: Primate intra-acrosomal sperm antigen for use in a contraceptive vaccine

US PAT NO: 5,695,932 [IMAGE AVAILABLE] L15: 10 of 21
TITLE: Telomerase activity assays for diagnosing pathogenic infections

US PAT NO: 5,645,986 [IMAGE AVAILABLE] L15: 11 of 21
TITLE: Therapy and diagnosis of conditions related to telomere length and/or telomerase activity

US PAT NO: 5,635,351 [IMAGE AVAILABLE] L15: 12 of 21
TITLE: Genetic gain and loss in gliomas

US PAT NO: 5,602,005 [IMAGE AVAILABLE] L15: 13 of 21
TITLE: Primate intra-acrosomal sperm antigen for use in a contraceptive vaccine

US PAT NO: 5,589,345 [IMAGE AVAILABLE] L15: 14 of 21
TITLE: Cultures of permanent lines of **human** promyelocytic cells and their uses for the screening of molecules utilizable in particular in the treatment of leukemias

US PAT NO: 5,571,698 [IMAGE AVAILABLE] L15: 15 of 21
TITLE: Directed evolution of novel binding proteins

US PAT NO: 5,487,970 [IMAGE AVAILABLE] L15: 16 of 21
TITLE: Compositions and methods for **detecting** gene rearrangements and **translocations**

US PAT NO: 5,480,784 [IMAGE AVAILABLE] L15: 17 of 21
TITLE: Nucleic acid sequence **amplification** methods

US PAT NO: 5,403,484 [IMAGE AVAILABLE] L15: 18 of 21
TITLE: Viruses expressing chimeric binding proteins

US PAT NO: 5,399,491 [IMAGE AVAILABLE] L15: 19 of 21
TITLE: Nucleic acid sequence **amplification** methods

US PAT NO: 5,242,795 [IMAGE AVAILABLE] L15: 20 of 21
TITLE: TCL-5 gene rearrangement involved in T-cell leukemia and melanoma

US PAT NO: 5,223,409 [IMAGE AVAILABLE] L15: 21 of 21
TITLE: Directed evolution of novel binding proteins

```
=> s l7 and 15(w)17

       1645633 15
       1336499 17
         11561 15(W)17
L16         17 L7 AND 15(W)17

=> d ti 1-17
```

US PAT NO: 5,928,900 [IMAGE AVAILABLE] L16: 1 of 17
TITLE: Bacterial exported proteins and acellular vaccines based thereon

US PAT NO: 5,843,642 [IMAGE AVAILABLE] L16: 2 of 17

TITLE: [redacted]hods for **detection** of acute pr[redacted]elocytic leukemia (APL)

US PAT NO: 5,830,462 [IMAGE AVAILABLE] L16: 3 of 17
TITLE: Regulated transcription of targeted genes and other biological events

US PAT NO: 5,807,836 [IMAGE AVAILABLE] L16: 4 of 17
TITLE: Interferon regulatory factors 1 and 2 in the diagnosis of tumorigenicity

US PAT NO: 5,783,666 [IMAGE AVAILABLE] L16: 5 of 17
TITLE: APC (adenomatous polyosis coli) protein

US PAT NO: 5,767,252 [IMAGE AVAILABLE] L16: 6 of 17
TITLE: Neuronal cell growth factor, Narp

US PAT NO: 5,753,231 [IMAGE AVAILABLE] L16: 7 of 17
TITLE: Primate intra-acrosomal sperm antigen for use in a contraceptive vaccine

US PAT NO: 5,712,149 [IMAGE AVAILABLE] L16: 8 of 17
TITLE: Chimeric receptor molecules for delivery of co-stimulatory signals

US PAT NO: 5,691,454 [IMAGE AVAILABLE] L16: 9 of 17
TITLE: APC antibodies

US PAT NO: 5,652,095 [IMAGE AVAILABLE] L16: 10 of 17
TITLE: Interferon regulatory factors 1 and 2 in the diagnosis of tumorigenicity

US PAT NO: 5,648,212 [IMAGE AVAILABLE] L16: 11 of 17
TITLE: **Detection** of inherited and somatic mutations of APC gene in colorectal cancer of **humans**

US PAT NO: 5,633,136 [IMAGE AVAILABLE] L16: 12 of 17
TITLE: ALL-1 polynucleotides for leukemia **detection** and treatment

US PAT NO: 5,633,135 [IMAGE AVAILABLE] L16: 13 of 17
TITLE: Chimeric nucleic acids and proteins resulting from ALL-1 region **chromosome** abnormalities

US PAT NO: 5,602,005 [IMAGE AVAILABLE] L16: 14 of 17
TITLE: Primate intra-acrosomal sperm antigen for use in a contraceptive vaccine

US PAT NO: 5,589,345 [IMAGE AVAILABLE] L16: 15 of 17
TITLE: Cultures of permanent lines of **human** promyelocytic cells and their uses for the screening of molecules utilizable in particular in the treatment of leukemias

US PAT NO: 5,567,586 [IMAGE AVAILABLE] L16: 16 of 17
TITLE: Methods of indentifying solid tumors with **chromosome** abnormalities in the ALL-1 region

US PAT NO: 5,401,835 [IMAGE AVAILABLE] L16: 17 of 17
TITLE: **Human** erythroid p55 nucleic acids

=> s l7 and intracromosom? (w) translocat?

0 INTRACROMOSOM?
3622 TRANSLOCAT?
0 INTRACROMOSOM? (W) TRANSLOCAT?

```
L17             0 [redacted] AND INTRACROMOSOM? (W) TRANSL[redacted]T?

=> s l7 and intrachromasom? (w) translocat?

             0 INTRACHROMASOM?
          3622 TRANSLOCAT?
             0 INTRACHROMASOM? (W) TRANSLOCAT?
L18          0 L7 AND INTRACHROMASOM? (W) TRANSLOCAT?

=> s RNA and amplif? and buffer and (ph (w) 6.5 or ph(w)7 or ph(w) 7.5 or
ph(w) 8 or ph(w) 8.5) and 150mm(w)salt

         19337 RNA
          3392 RNAS
         19467 RNA
                 (RNA OR RNAS)
        262639 AMPLIF?
        192027 BUFFER
         65440 BUFFERS
        209132 BUFFER
                 (BUFFER OR BUFFERS)
        230121 PH
          3229 PHS
        230653 PH
                 (PH OR PHS)
         92831 6.5
          8540 PH (W) 6.5
        230121 PH
          3229 PHS
        230653 PH
                 (PH OR PHS)
       2098561 7
         16911 PH(W)7
        230121 PH
          3229 PHS
        230653 PH
                 (PH OR PHS)
        122997 7.5
         17023 PH(W) 7.5
        230121 PH
          3229 PHS
        230653 PH
                 (PH OR PHS)
       1989504 8
         10883 PH(W) 8
        230121 PH
          3229 PHS
        230653 PH
                 (PH OR PHS)
         73315 8.5
          6728 PH(W) 8.5
           280 150MM
        268744 SALT
        239774 SALTS
        331930 SALT
                 (SALT OR SALTS)
             0 150MM(W)SALT
L19          0 RNA AND AMPLIF? AND BUFFER AND (PH (W) 6.5 OR PH(W)7 OR PH(
W)
               7.5 OR PH(W) 8 OR PH(W) 8.5) AND 150MM(W)SALT

=> s RNA and amplif? and buffer and (ph (w) 6.5 or ph(w)7 or ph(w) 7.5 or
ph(w) 8 or ph(w) 8.5)

         19337 RNA
```

```
         3392 R[redacted]
        19467 R[redacted]
                (RNA OR RNAS)
       262639 AMPLIF?
       192027 BUFFER
        65440 BUFFERS
       209132 BUFFER
                (BUFFER OR BUFFERS)
       230121 PH
         3229 PHS
       230653 PH
                (PH OR PHS)
        92831 6.5
         8540 PH (W) 6.5
       230121 PH
         3229 PHS
       230653 PH
                (PH OR PHS)
      2098561 7
        16911 PH(W)7
       230121 PH
         3229 PHS
       230653 PH
                (PH OR PHS)
       122997 7.5
        17023 PH(W) 7.5
       230121 PH
         3229 PHS
       230653 PH
                (PH OR PHS)
      1989504 8
        10883 PH(W) 8
       230121 PH
         3229 PHS
       230653 PH
                (PH OR PHS)
        73315 8.5
         6728 PH(W) 8.5
L20       4967 RNA AND AMPLIF? AND BUFFER AND (PH (W) 6.5 OR PH(W)7 OR PH(
W)
                7.5 OR PH(W) 8 OR PH(W) 8.5)

=> s l20 and non(w)ionic and detergent

       920721 NON
           13 NONS
       920724 NON
                (NON OR NONS)
        68064 IONIC
         1089 IONICS
        68560 IONIC
                (IONIC OR IONICS)
        25653 NON(W)IONIC
        32959 DETERGENT
        27255 DETERGENTS
        46476 DETERGENT
                (DETERGENT OR DETERGENTS)
L21         287 L20 AND NON(W)IONIC AND DETERGENT

=> s l21 and solid

       641472 SOLID
       148160 SOLIDS
       688602 SOLID
                (SOLID OR SOLIDS)
```

```
L22          238 L[redacted]AND SOLID

=> s l22 and 150mm

             280 150MM
L23            0 L22 AND 150MM

=> s l22 and 150(w)mm

          511498 150
          433330 MM
            1368 MMS
          433917 MM
                 (MM OR MMS)
           17854 150(W)MM
L24          114 L22 AND 150(W)MM

=> s l24 and separat?

         1316790 SEPARAT?
L25          113 L24 AND SEPARAT?

=> s l25 and immobil? and wash

           44876 IMMOBIL?
           77208 WASH
           17496 WASHES
           85358 WASH
                 (WASH OR WASHES)
L26           60 L25 AND IMMOBIL? AND WASH

=> s l26 and hybridiz?

           17335 HYBRIDIZ?
L27           50 L26 AND HYBRIDIZ?

=> s l27 and blood

          107708 BLOOD
             296 BLOODS
          107735 BLOOD
                 (BLOOD OR BLOODS)
L28           43 L27 AND BLOOD

=> s l28 and plasma

           85075 PLASMA
            3708 PLASMAS
           85382 PLASMA
                 (PLASMA OR PLASMAS)
L29           26 L28 AND PLASMA

=> s l29 and bone marrow

           35620 BONE
           10228 BONES
           39191 BONE
                 (BONE OR BONES)
            7537 MARROW
             247 MARROWS
            7700 MARROW
                 (MARROW OR MARROWS)
            6755 BONE MARROW
                 (BONE(W)MARROW)
L30           13 L29 AND BONE MARROW
```

=> d ti 1-13

US PAT NO: 5,919,637 [IMAGE AVAILABLE] L30: 1 of 13
TITLE: Method for identifying reduced binding between GMP-140 and GMP-140 ligand

US PAT NO: 5,874,234 [IMAGE AVAILABLE] L30: 2 of 13
TITLE: Assay for a novel mammalian protein associated with uncontrolled cell division

US PAT NO: 5,843,669 [IMAGE AVAILABLE] L30: 3 of 13
TITLE: Cleavage of nucleic acid acid using thermostable methoanococcus jannaschii FEN-1 endonucleases

US PAT NO: 5,804,440 [IMAGE AVAILABLE] L30: 4 of 13
TITLE: Human neutralizing monoclonal antibodies to human immunodeficiency virus

US PAT NO: 5,767,241 [IMAGE AVAILABLE] L30: 5 of 13
TITLE: Soluble form of GMP-140

US PAT NO: 5,756,676 [IMAGE AVAILABLE] L30: 6 of 13
TITLE: Mammalian protein associated with uncontrolled cell division

US PAT NO: 5,734,022 [IMAGE AVAILABLE] L30: 7 of 13
TITLE: Antibodies to a novel mammalian protein associated with uncontrolled cell division

US PAT NO: 5,726,018 [IMAGE AVAILABLE] L30: 8 of 13
TITLE: Nucleic acid based assays to detect a novel mammalian protein associated with uncontrolled cell division

US PAT NO: 5,717,072 [IMAGE AVAILABLE] L30: 9 of 13
TITLE: Antibodies that are immunoreactive with interleukin-4 receptors

US PAT NO: 5,652,138 [IMAGE AVAILABLE] L30: 10 of 13
TITLE: Human neutralizing monoclonal antibodies to human immunodeficiency virus

US PAT NO: 5,645,986 [IMAGE AVAILABLE] L30: 11 of 13
TITLE: Therapy and diagnosis of conditions related to telomere length and/or telomerase activity

US PAT NO: 5,482,834 [IMAGE AVAILABLE] L30: 12 of 13
TITLE: Evaluation of nucleic acids in a biological sample **hybridization** in a solution of chaotrophic salt solubilized cells

US PAT NO: 5,378,464 [IMAGE AVAILABLE] L30: 13 of 13
TITLE: Modulation of inflammatory responses by administration of GMP-140 or antibody to GMP-140

=> d his

(FILE 'USPAT' ENTERED AT 11:13:18 ON 10 AUG 1999)
L1 1648 S CHROMOSOM? AND TRANSLOCAT?
L2 2 S L1 AND T(W)1(W)19
L3 0 S L1 AND T(W)2(W)5
L4 0 S L1 AND T(W)2(W)13
L5 37 S L1 AND 4(W)11

```
L6          1456 S [illegible] AND HUMAN
L7          1042 S [illegible] AND DETECT? AND AMPLIF?
L8            28 S L7 AND 6(W)9
L9             5 S L7 AND 8(W)21
L10           28 S L7 AND 9(W)11
L11           18 S L7 AND 11(W)14
L12            7 S L7 AND 11(W)19
L13            4 S L7 AND 11 (W)22
L14            8 S L7 AND 12(W)21
L15           21 S L7 AND 14(W)18
L16           17 S L7 AND 15(W)17
L17            0 S L7 AND INTRACROMOSOM? (W) TRANSLOCAT?
L18            0 S L7 AND INTRACHROMASOM? (W) TRANSLOCAT?
L19            0 S RNA AND AMPLIF? AND BUFFER AND (PH (W) 6.5 OR PH(W)7 OR
PH(
L20         4967 S RNA AND AMPLIF? AND BUFFER AND (PH (W) 6.5 OR PH(W)7 OR
PH(
L21          287 S L20 AND NON(W)IONIC AND DETERGENT
L22          238 S L21 AND SOLID
L23            0 S L22 AND 150MM
L24          114 S L22 AND 150(W)MM
L25          113 S L24 AND SEPARAT?
L26           60 S L25 AND IMMOBIL? AND WASH
L27           50 S L26 AND HYBRIDIZ?
L28           43 S L27 AND BLOOD
L29           26 S L28 AND PLASMA
L30           13 S L29 AND BONE MARROW

=> s l24 and (blood or plasma or bone marrow)

        107708 BLOOD
           296 BLOODS
        107735 BLOOD
                 (BLOOD OR BLOODS)
         85075 PLASMA
          3708 PLASMAS
         85382 PLASMA
                 (PLASMA OR PLASMAS)
         35620 BONE
         10228 BONES
         39191 BONE
                 (BONE OR BONES)
          7537 MARROW
           247 MARROWS
          7700 MARROW
                 (MARROW OR MARROWS)
          6755 BONE MARROW
                 (BONE(W)MARROW)
L31         104 L24 AND (BLOOD OR PLASMA OR BONE MARROW)

=> d ti 1-104

                                                          L31: 1 of 104
US PAT NO:      5,928,905 [IMAGE AVAILABLE]
TITLE:          End-complementary polymerase reaction

                                                          L31: 2 of 104
US PAT NO:      5,922,846 [IMAGE AVAILABLE]
TITLE:          Process for refolding recombinantly produced
                  TGF-.beta.-like proteins

                                                          L31: 3 of 104
US PAT NO:      5,919,637 [IMAGE AVAILABLE]
TITLE:          Method for identifying reduced binding between GMP-140 and
                  GMP-140 ligand

                                                          L31: 4 of 104
US PAT NO:      5,914,237 [IMAGE AVAILABLE]
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TITLE: Kinase receptor activation assay

US PAT NO: 5,891,650 [IMAGE AVAILABLE] L31: 5 of 104
TITLE: Kinase receptor activation assay

US PAT NO: 5,888,780 [IMAGE AVAILABLE] L31: 6 of 104
TITLE: Rapid detection and identification of nucleic acid variants

US PAT NO: 5,885,768 [IMAGE AVAILABLE] L31: 7 of 104
TITLE: Hepatitis E virus peptide antigen and antibodies

US PAT NO: 5,877,012 [IMAGE AVAILABLE] L31: 8 of 104
TITLE: Class of proteins for the control of plant pests

US PAT NO: 5,874,561 [IMAGE AVAILABLE] L31: 9 of 104
TITLE: DNA, host cell and vector encoding a protein with cytokine inhibitory activity

US PAT NO: 5,874,283 [IMAGE AVAILABLE] L31: 10 of 104
TITLE: Mammalian flap-specific endonuclease

US PAT NO: 5,874,234 [IMAGE AVAILABLE] L31: 11 of 104
TITLE: Assay for a novel mammalian protein associated with uncontrolled cell division

US PAT NO: 5,872,217 [IMAGE AVAILABLE] L31: 12 of 104
TITLE: Antibodies which specifically bind a cancer related antigen

US PAT NO: 5,866,341 [IMAGE AVAILABLE] L31: 13 of 104
TITLE: Compositions and methods for screening drug libraries

US PAT NO: 5,864,011 [IMAGE AVAILABLE] L31: 14 of 104
TITLE: Cancer related antigen

US PAT NO: 5,858,688 [IMAGE AVAILABLE] L31: 15 of 104
TITLE: Gro genes, proteins, and uses thereof

US PAT NO: 5,849,883 [IMAGE AVAILABLE] L31: 16 of 104
TITLE: Method for purifying granulocyte colony stimulating factor

US PAT NO: 5,846,824 [IMAGE AVAILABLE] L31: 17 of 104
TITLE: Polypeptides having kinase activity, their preparation and use

US PAT NO: 5,846,717 [IMAGE AVAILABLE] L31: 18 of 104
TITLE: Detection of nucleic acid sequences by invader-directed cleavage

US PAT NO: 5,843,707 [IMAGE AVAILABLE] L31: 19 of 104
TITLE: Nucleic acid encoding a novel P-selectin ligand protein

US PAT NO: 5,843,693 [IMAGE AVAILABLE] L31: 20 of 104
TITLE: Assay method for screening for inhibitors of proTNF conversion

US PAT NO: 5,843,669 [IMAGE AVAILABLE] L31: 21 of 104
TITLE: Cleavage of nucleic acid acid using thermostable methoanococcus jannaschii FEN-1 endonucleases

US PAT NO: 5,843,654 [IMAGE AVAILABLE] L31: 22 of 104
TITLE: Rapid detection of mutations in the p53 gene

US PAT NO: 5,840,679 [IMAGE AVAILABLE] L31: 23 of 104

TITLE: Method of inhibiting P-selectin ligand activity

US PAT NO: 5,837,450 [IMAGE AVAILABLE] L31: 24 of 104
TITLE: Detection of target nucleic acid molecules using thermostable 5' nuclease

US PAT NO: 5,834,290 [IMAGE AVAILABLE] L31: 25 of 104
TITLE: Recombinant stratum corneum chymotryptic enzyme (SCCE)

US PAT NO: 5,830,995 [IMAGE AVAILABLE] L31: 26 of 104
TITLE: Fanphiregulins: a family of heparin-binding epithelial cell growth factors

US PAT NO: 5,830,742 [IMAGE AVAILABLE] L31: 27 of 104
TITLE: TNF-.alpha. converting enzyme

US PAT NO: 5,830,721 [IMAGE AVAILABLE] L31: 28 of 104
TITLE: DNA mutagenesis by random fragmentation and reassembly

US PAT NO: 5,830,684 [IMAGE AVAILABLE] L31: 29 of 104
TITLE: Native type II GAP, methods for purifying various GAPs and uses of GAPs to diagnose cancer

US PAT NO: 5,830,644 [IMAGE AVAILABLE] L31: 30 of 104
TITLE: Method for screening for agents which increase telomerase activity in a cell

US PAT NO: 5,827,817 [IMAGE AVAILABLE] L31: 31 of 104
TITLE: P-selectin ligand protein

US PAT NO: 5,824,492 [IMAGE AVAILABLE] L31: 32 of 104
TITLE: Polypeptides having kinase activity, their preparation and use

US PAT NO: 5,811,238 [IMAGE AVAILABLE] L31: 33 of 104
TITLE: Methods for generating polynucleotides having desired characteristics by iterative selection and recombination

US PAT NO: 5,804,440 [IMAGE AVAILABLE] L31: 34 of 104
TITLE: Human neutralizing monoclonal antibodies to human immunodeficiency virus

US PAT NO: 5,795,763 [IMAGE AVAILABLE] L31: 35 of 104
TITLE: Synthesis-deficient thermostable DNA polymerase

US PAT NO: 5,789,224 [IMAGE AVAILABLE] L31: 36 of 104
TITLE: Recombinant expression vectors and purification methods for thermus thermophilus DNA polymerase

US PAT NO: 5,776,694 [IMAGE AVAILABLE] L31: 37 of 104
TITLE: Diagnostic kits useful for selectively detecting microorganisms in samples

US PAT NO: 5,770,689 [IMAGE AVAILABLE] L31: 38 of 104
TITLE: Hepatitis E virus ORF Z peptides

US PAT NO: 5,767,241 [IMAGE AVAILABLE] L31: 39 of 104
TITLE: Soluble form of GMP-140

US PAT NO: 5,766,863 [IMAGE AVAILABLE] L31: 40 of 104
TITLE: Kinase receptor activation assay

US PAT NO: 5,763,573 [IMAGE AVAILABLE] L31: 41 of 104
TITLE: GTPase activating protein fragments

US PAT NO: 5,760,203 [IMAGE AVAILABLE] L31: 42 of 104
TITLE: [redacted] gene sequences

US PAT NO: 5,759,791 [IMAGE AVAILABLE] L31: 43 of 104
TITLE: Cancer related antigen

US PAT NO: 5,756,696 [IMAGE AVAILABLE] L31: 44 of 104
TITLE: Compositions for chromosome-specific staining

US PAT NO: 5,756,676 [IMAGE AVAILABLE] L31: 45 of 104
TITLE: Mammalian protein associated with uncontrolled cell division

US PAT NO: 5,741,490 [IMAGE AVAILABLE] L31: 46 of 104
TITLE: Hepatitis E virus vaccine and method

US PAT NO: 5,736,340 [IMAGE AVAILABLE] L31: 47 of 104
TITLE: Secreted Mac-2-binding glycoprotein

US PAT NO: 5,734,022 [IMAGE AVAILABLE] L31: 48 of 104
TITLE: Antibodies to a novel mammalian protein associated with uncontrolled cell division

US PAT NO: 5,731,426 [IMAGE AVAILABLE] L31: 49 of 104
TITLE: Phaseolus .alpha.-D-galactosidases

US PAT NO: 5,726,018 [IMAGE AVAILABLE] L31: 50 of 104
TITLE: Nucleic acid based assays to detect a novel mammalian protein associated with uncontrolled cell division

US PAT NO: 5,719,028 [IMAGE AVAILABLE] L31: 51 of 104
TITLE: Cleavase fragment length polymorphism

US PAT NO: 5,717,072 [IMAGE AVAILABLE] L31: 52 of 104
TITLE: Antibodies that are immunoreactive with interleukin-4 receptors

US PAT NO: 5,715,835 [IMAGE AVAILABLE] L31: 53 of 104
TITLE: Methods for treating and reducing the potential for cardiovascular disease using methioninase compositions

US PAT NO: 5,700,636 [IMAGE AVAILABLE] L31: 54 of 104
TITLE: Methods for selectively detecting microorganisms associated with vaginal infections in complex biological samples

US PAT NO: 5,691,142 [IMAGE AVAILABLE] L31: 55 of 104
TITLE: Detection of target nucleic acid molecules using synthesis-deficient thermostable DNA polymerase

US PAT NO: 5,690,929 [IMAGE AVAILABLE] L31: 56 of 104
TITLE: Use of methioninase and chemotherapy agents in chemotherapy

US PAT NO: 5,681,755 [IMAGE AVAILABLE] L31: 57 of 104
TITLE: Method for depositing metal particles on a marker

US PAT NO: 5,674,755 [IMAGE AVAILABLE] L31: 58 of 104
TITLE: Method for depositing metal particles on a marker

US PAT NO: 5,665,874 [IMAGE AVAILABLE] L31: 59 of 104
TITLE: Cancer related antigen

US PAT NO: 5,661,025 [IMAGE AVAILABLE] L31: 60 of 104
TITLE: Self-assembling polynucleotide delivery system comprising

dendrimer polycations

US PAT NO: 5,656,731 [IMAGE AVAILABLE] L31: 61 of 104
TITLE: Nucleic acid-**amplified** immunoassay probes

US PAT NO: 5,654,418 [IMAGE AVAILABLE] L31: 62 of 104
TITLE: Nucleic acid probes useful for detecting microorganisms associated with vaginal infections

US PAT NO: 5,652,138 [IMAGE AVAILABLE] L31: 63 of 104
TITLE: Human neutralizing monoclonal antibodies to human immunodeficiency virus

US PAT NO: 5,650,494 [IMAGE AVAILABLE] L31: 64 of 104
TITLE: Process for refolding recombinantly produced TGF-.beta.-like proteins

US PAT NO: 5,645,986 [IMAGE AVAILABLE] L31: 65 of 104
TITLE: Therapy and diagnosis of conditions related to telomere length and/or telomerase activity

US PAT NO: 5,644,035 [IMAGE AVAILABLE] L31: 66 of 104
TITLE: Method for purifying secreted Mac-2-binding glycoprotein

US PAT NO: 5,624,833 [IMAGE AVAILABLE] L31: 67 of 104
TITLE: Purified thermostable nucleic acid polymerase enzyme from Thermotoga maritima

US PAT NO: 5,624,809 [IMAGE AVAILABLE] L31: 68 of 104
TITLE: Device for immunochromatographic analysis

US PAT NO: 5,622,931 [IMAGE AVAILABLE] L31: 69 of 104
TITLE: Human tissue factor related DNA segments, polypeptides and antibodies

US PAT NO: 5,618,711 [IMAGE AVAILABLE] L31: 70 of 104
TITLE: Recombinant expression vectors and purification methods for Thermus thermophilus DNA polymerase

US PAT NO: 5,614,402 [IMAGE AVAILABLE] L31: 71 of 104
TITLE: 5' nucleases derived from thermostable DNA polymerase

US PAT NO: 5,606,042 [IMAGE AVAILABLE] L31: 72 of 104
TITLE: Glycine .alpha.-D-galactosidases

US PAT NO: 5,605,824 [IMAGE AVAILABLE] L31: 73 of 104
TITLE: Composition for hybridizing nucleic acids using single-stranded nucleic acid binding protein

US PAT NO: 5,583,010 [IMAGE AVAILABLE] L31: 74 of 104
TITLE: Nucleic acid molecule encoding the porcine growth hormone receptor

US PAT NO: 5,582,986 [IMAGE AVAILABLE] L31: 75 of 104
TITLE: Antisense oligonucleotide inhibition of the ras gene

US PAT NO: 5,541,311 [IMAGE AVAILABLE] L31: 76 of 104
TITLE: Nucleic acid encoding synthesis-deficient thermostable DNA polymerase

US PAT NO: 5,498,538 [IMAGE AVAILABLE] L31: 77 of 104
TITLE: Totally synthetic affinity reagents

US PAT NO: 5,491,098 [IMAGE AVAILABLE] L31: 78 of 104
TITLE: Method for depositing metal particles on a marker

US PAT NO: 5,[redacted],834 [IMAGE AVAILABLE] L31: 79 of 104
TITLE: Evaluation of nucleic acids in a biological sample hybridization in a solution of chaotrophic salt solubilized cells

US PAT NO: 5,470,569 [IMAGE AVAILABLE] L31: 80 of 104
TITLE: Recombinant colony stimulating factor-1

US PAT NO: 5,468,647 [IMAGE AVAILABLE] L31: 81 of 104
TITLE: Method for immunochromatographic analysis

US PAT NO: 5,455,330 [IMAGE AVAILABLE] L31: 82 of 104
TITLE: Interleukin-1 antagonist and uses thereof

US PAT NO: 5,451,507 [IMAGE AVAILABLE] L31: 83 of 104
TITLE: Method for immunochromatographic analysis

US PAT NO: 5,437,864 [IMAGE AVAILABLE] L31: 84 of 104
TITLE: Method of inhibiting **blood** coagulation in extracorporeal circulation by inhibiting human tissue factor

US PAT NO: 5,420,029 [IMAGE AVAILABLE] L31: 85 of 104
TITLE: Mutated thermostable nucleic acid polymerase enzyme from thermotoga maritima

US PAT NO: 5,378,464 [IMAGE AVAILABLE] L31: 86 of 104
TITLE: Modulation of inflammatory responses by administration of GMP-140 or antibody to GMP-140

US PAT NO: 5,374,553 [IMAGE AVAILABLE] L31: 87 of 104
TITLE: DNA encoding a thermostable nucleic acid polymerase enzyme from thermotoga maritima

US PAT NO: 5,352,600 [IMAGE AVAILABLE] L31: 88 of 104
TITLE: Purified thermostable enzyme

US PAT NO: 5,334,513 [IMAGE AVAILABLE] L31: 89 of 104
TITLE: Method for immunochromatographic analysis

US PAT NO: 5,248,619 [IMAGE AVAILABLE] L31: 90 of 104
TITLE: Device and kit for immunochromatographic analysis

US PAT NO: 5,231,168 [IMAGE AVAILABLE] L31: 91 of 104
TITLE: Malaria antigen

US PAT NO: 5,223,427 [IMAGE AVAILABLE] L31: 92 of 104
TITLE: Hybridomas producing monoclonal antibodies reactive with human tissue-factor glycoprotein heavy chain

US PAT NO: 5,215,909 [IMAGE AVAILABLE] L31: 93 of 104
TITLE: Human cholinesterase genes

US PAT NO: 5,164,294 [IMAGE AVAILABLE] L31: 94 of 104
TITLE: Method for immunochromatographic analysis

US PAT NO: 5,110,730 [IMAGE AVAILABLE] L31: 95 of 104
TITLE: Human tissue factor related DNA segments

US PAT NO: 5,104,650 [IMAGE AVAILABLE] L31: 96 of 104
TITLE: Uses of recombinant colony stimulating factor-1

US PAT NO: 5,079,352 [IMAGE AVAILABLE] L31: 97 of 104
TITLE: Purified thermostable enzyme

US PAT NO: 5,[redacted],607 [IMAGE AVAILABLE] L31: 98 of 104
TITLE: Method for immunochromatographic analysis

US PAT NO: 4,959,314 [IMAGE AVAILABLE] L31: 99 of 104
TITLE: Cysteine-depleted muteins of biologically active proteins

US PAT NO: 4,891,324 [IMAGE AVAILABLE] L31: 100 of 104
TITLE: Particle with luminescer for assays

US PAT NO: 4,889,818 [IMAGE AVAILABLE] L31: 101 of 104
TITLE: Purified thermostable enzyme

US PAT NO: 4,847,201 [IMAGE AVAILABLE] L31: 102 of 104
TITLE: DNA encoding for CSF-1 and accompanying recombinant systems

US PAT NO: 4,784,941 [IMAGE AVAILABLE] L31: 103 of 104
TITLE: Expression and diagnostic use of pENV-3 encoded peptides which are immunologically reactive with antibodies to LAV

US PAT NO: 4,735,800 [IMAGE AVAILABLE] L31: 104 of 104
TITLE: Vaccines against rift valley fever virus

09064643 97292[redacted]
Myxoid chondr[redacted]arcoma (chordoid sarcoma) of b[redacted]e: a report of two cases and **review** of the literature.
Kilpatrick SE; Inwards CY; Fletcher CD; Smith MA; Gitelis S
Department of Pathology, Wake Forest University Medical Center, Bowman Gray School of Medicine, Winston-Salem, North Carolina 27157-1072, USA.
Cancer (UNITED STATES) May 15 1997, 79 (10) p1903-10, ISSN 0008-543X Journal Code: CLZ
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW OF REPORTED CASES
BACKGROUND: Chondrosarcoma of bone is a well recognized, relatively common clinicopathologic entity. Morphologically distinct soft tissue chordoid sarcoma (CS), or extraskeletal myxoid chondrosarcoma, is a relatively rare tumor that has generally been documented in extraosseous soft tissues. METHODS: The clinical and pathologic features of two patients with biopsy-proven CS from the pathology files of the Mayo Clinic and St. Thomas's Hospital were evaluated. Routine hematoxylin and eosin-stained slides were reviewed in both cases. Sections from both were examined immunohistochemically using the avidin-biotin-peroxidase technique and employing commercially available antibodies to the following antigens: S-100 protein, cytokeratin (AE1/AE3), epithelial membrane antigen (EMA), CD31, and factor VIII. Appropriate positive and negative controls were utilized throughout these procedures. Cytogenetic analysis was performed on fresh samples obtained from one tumor. Clinical data were obtained from the patients' medical records. RESULTS: The two cases of primary CS of bone arose from the right distal femur and right scapula, respectively, in 2 men ages 48 and 76 years, respectively. Morphologically, the tumors were lobulated, multinodular, and comprised of a uniform population of rounded to slightly spindled cells. Nuclei were hyperchromatic with inconspicuous nucleoli and surrounded by clear, vacuolated to eosinophilic cytoplasm. Neoplastic cells were arranged in anastomosing chords, strands, and, less often, nests and pseudopapillary structures embedded in an abundant, mostly hypovascular, mucinous matrix. Foci of hemorrhage and cystic degeneration were present in both tumors. No well developed hyaline cartilage or neoplastic osteoid was observed. Immunohistochemically, one neoplasm showed focal positivity for S-100 protein but was uniformly negative for cytokeratin (AE1/AE3), factor VIII, and CD31. The other tumor showed no immunopositivity with cytokeratin, EMA, or S-100 protein. Cytogenetic analysis in the latter tumor revealed a nonrandom reciprocal **chromosomal translocation**, t(**9;22**)(q22-31;q11-12).
Both patients developed local recurrences and widespread distant metastases. Wide surgical excision was the primary mode of therapy. One patient died of tumor. CONCLUSIONS: Skeletal CS is an extraordinarily rare neoplasm with a distinct morphology. Although follow-up data were limited to only four examples, including two from the literature, the clinical course appears worse than that for usual chondrosarcoma of bone. Wide surgical resection appears to represent the best mode of therapy. The role of chemotherapy and radiation therapy has not been clearly defined.

4/3,AB/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08542047 96141136
Detection of **chromosomal translocations** in leukemia-lymphoma cells by polymerase chain reaction.
Drexler HG; Borkhardt A; Janssen JW
DSM-German Collection of Microorganisms and Cell Cultures, Department of Human and Animal Cell Cultures, Braunschweig, Germany.
Leuk Lymphoma (SWITZERLAND) Nov 1995, 19 (5-6) p359-80, ISSN 1042-8194 Journal Code: BNQ
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, ACADEMIC
In recent years many **chromosomal translocations** involved in

Repp R; Kreud[illegible] J; Buchen U; Lampert F(a)
AUTHOR ADDRESS: (a)Dep. Pediatr. Hematol. Oncol [illegible]niv. Giessen, Feulgenstrasse 12, D-35385 Giessen, Germany

JOURNAL: Leukemia (Basingstoke) 9 (4):p719-722 1995
ISSN: 0887-6924
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

RC 643.L49

ABSTRACT: A number of gene arrangements have been described as characteristic abnormalities associated with different types of leukemia, and this list is still growing. In view of the biological, clinical and prognostic relevance of the pathological fusion products, techniques permitting their detection are of paramount importance in the clinical setting. In some instances, permanent leukemic cell lines carrying the abnormality of Interest are available for the establishment and standardization of molecular assays. For a number of newly discovered gene rearrangements, however, this may not be the case. It is therefore of great interest for clinical laboratories to have alternative technical possibilities for the set-up of standardized molecular tests. This problem provided the stimulus to design a simple and rapid method for in vitro generation of chimeric **RNA** molecules corresponding to pathological fusion transcripts typical for **chromosomal translocations** in leukemias. Two separate fragments are generated in a four-primer multiplex PCR. Due to a PCR-generated overlap, a chimeric fragment can be synthesized in a second round of PCR. This PCR product is then **purified** with the help of magnetic beads. Due to the SP6 promotor sequence incorporated during the second round of PCR, transcription into **RNA** is easily facilitated while the template DNA is still bound to the solid phase. Following this strategy we were able to synthesize the fusion transcripts m-BCR/ABL, CBF-beta/MYH11, and MLL/AFp1 which are the molecular equivalents of t(9;22)(q34,q11), inv16(p13;q22) and t(1;11)(p32;q23), respectively. The chimeric **RNA** will be useful as a control template in diagnostic RT-PCR strategies. It can also be further processed in translation systems leading to the corresponding chimeric oncoprotein. This approach can be easily used to create any hybrid **RNA** of interest.

2/3,AB/19 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09039267 BIOSIS NO.: 199497047637
The HOX-11 (TCL-3) homeobox proto-oncogene encodes a nuclear protein that undergoes cell cycle-dependent regulation.

AUTHOR: Zhang Nan; Going Zhen-Zhen; Minden Mark; Lu Ming(a)
AUTHOR ADDRESS: (a)Northeaster Ontario Regional Cancer Centre, Dep. Med., Univ. Ottawa, 41 Ramsey Lake Road, Sudbur, Canada

JOURNAL: Oncogene 8 (12):p3265-3270 1993
ISSN: 0950-9232
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Molecular analysis of the t(10;14) **chromosomal translocation** found in pediatric patients with T-cell acute lymphoblastic leukemia has led to the identification of the HOX-11 (TCL-3) protooncogene. The HOX-11 cDNA contains an open reading frame encoding a homeoprotein with features of DNA-binding. The majority of the t(10;14) **chromosomal translocation** breakpoints have been mapped to the 5' end of the HOX-11 gene, supporting the notion that

AML1) are the most frequent [redacted] **translocations** [redacted] acute leukemias in humans. We [redacted]d others previously demonstrated that homozygous disruption of the mouse Cbfa2 (AML1) gene results in embryonic lethality at midgestation due to hemorrhaging in the central nervous system and blocks fetal liver hematopoiesis. Here we demonstrate that homozygous mutation of the Cbfb gene results in the same phenotype. Our results demonstrate that the CBFbeta subunit is required for CBFalpha2 function in vivo.

2/3,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08122630 95171612
Detection of Philadelphia **chromosome** using PCR and europium-labeled DNA probes.
Eskola JU; Hamalainen M; Nanto V; Rajamaki A; Dahlen P; Iitia A; Siitari H
Joint Clinical Biochemistry Laboratory, University of Turku, Turku University Hospital, Finland.
Clin Biochem (UNITED STATES) Oct 1994, 27 (5) p373-9, ISSN 0009-9120 Journal Code: DBV
Languages: ENGLISH
Document type: JOURNAL ARTICLE
QP501.C5?
More than 95% of the patients with chronic myelogenous leukemia (CML) carry **translocations** between protooncogene abl of **chromosome** 9 and bcr gene of **chromosome** 22, resulting in the Philadelphia **chromosome** (Ph1). After allogeneic **bone marrow** transplantation (BMT) it is important to detect possible residual malignant cells in CML patients. A new sensitive hybridization method combined with polymerase chain reaction (PCR), based on the detection of the europium (Eu3+) label by time-resolved fluorescence, was applied for the detection of Ph1 **chromosome**. Total **RNA** from 10(6) peripheral **blood** leukocytes was isolated by the acid guanidinium thiocyanate-phenol-chloroform extraction. After cDNA synthesis by reverse transcriptase, the PCR amplification (30 cycles) was carried out. In the detection phase two oligonucleotide probes were used in the hybridization reaction, one biotinylated (bcr gene, exon 2) and one (abl gene) labeled with Eu3+. The hybrids were collected in a streptavidin-coated microtitration well and the bound Eu3+ was measured in a time-resolved fluorometer. To assess the sensitivity of the method, different numbers of CML cell line K562 cells were mixed with 10(5) apparently normal human leukocytes. Five K562 cells/10(5) leukocytes could be detected. Six patients with CML confirmed by clinical and cytogenetic criteria were studied. Three of the patients underwent an allogeneic BTM 6-18 months before the investigation and all of them were Ph1-negative. The other three patients who were nontransplanted were positive as expected.

2/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07821655 94052146
An ets-related gene, ERG, is rearranged in human myeloid leukemia with t(16;21) **chromosomal translocation**.
Shimizu K; Ichikawa H; Tojo A; Kaneko Y; Maseki N; Hayashi Y; Ohira M; Asano S; Ohki M
Department of Immunology and Virology, Saitama Cancer Center Research Institute, Japan.
Proc Natl Acad Sci U S A (UNITED STATES) Nov 1 1993, 90 (21) p10280-4, ISSN 0027-8424 Journal Code: PV3
Languages: ENGLISH
Document type: JOURNAL ARTICLE

transcription suggests that one or more of the ELL-associated proteins regulate this activity, possibly through an interaction with the N-terminal domain of the ELL protein, which was shown to be required for the transcriptional inhibitory activity of ELL. Characterization of these ELL interacting proteins should help define the regulation of the biochemical activities of ELL and how loss of this regulation leads to the development of acute myeloid leukemia.

2/3,AB/17 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09860247 BIOSIS NO.: 199598315165
Specific Binding of Leukemia Oncogene Fusion Protein Peptides to HLA Class I Molecules.

AUTHOR: Bocchia Monica; Wentworth Peggy A; Southwood Scott; Sidney John; McGraw Kimberly; Scheinberg David A(a); Sette Alessandro
AUTHOR ADDRESS: (a)Memorial Sloan Kettering Cancer Cent., 1275 York Ave., New York, NY 10021, USA

JOURNAL: Blood 85 (10):p2680-2684 1995
ISSN: 0006-4971
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Many human leukemias are characterized by **chromosomal translocations** yielding hybrid RNAs capable of encoding fusion chimeric proteins. The unique amino acid sequences found in these oncogenic fusion proteins represent true tumor-specific antigens that are potentially immunogenic. Although these leukemia-specific fusion proteins have an intracellular location, they might be recognized immunologically by T lymphocytes if peptides derived from the unique sequences are capable of presentation by the major histocompatibility complex (MHC) molecules on leukemic cells. The ability of a series of synthetic peptides corresponding to the junctional sequences of chronic myelogenous leukemia (CML)-derived bcr-abl and acute promyelocytic leukemia (APL)-derived PML-RAR-alpha fusion proteins to bind to **purified** class I molecules was studied. A series of 152 peptides 8, 9, 10, and 11 amino acids in length, spanning the b3a2 and b2a2 breakpoints for CML and PML-RAR-alpha A and B breakpoints for APL were analyzed for HLA A1, A2.1, A3.2, A11, A24, B7, BS, and 827 binding motifs. Twenty-one CML peptides and 4 APL peptides were predicted to be potential HLA class I binders. The peptides were tested for binding to appropriate **purified** HLA molecules in a competition radioimmunoassay. Four peptides derived from b3a2 CML breakpoint bound with high (lt 50 nmol/L) or intermediate (ltoreq 500 nmol/L) affinity to HLA A3, A11, and BS. None of the CML b2a2 or PML-RAR-alpha A or B junctional peptides showed affinity of this magnitude for the HLA class I molecules tested. This is the first evidence that tumor-specific breakpoint peptides can bind human MHC class I molecules and provides a rationale for developing a therapeutic vaccine strategy.

2/3,AB/18 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09820881 BIOSIS NO.: 199598275799
Rapid synthesis of hybrid **RNA** molecules associated with leukemia-specific **chromosomal translocations**.

AUTHOR: Borkhardt A; Mitteis M; Brettreich S; Schlieben S; Hammermann J;

deregulation of the HOX-11 gene by the t(10;1[redacted]chromosomal **translocatio**[redacted] contributed importantly to leuk[redacted]a formation. To further define the role of the HOX-11 homeoprotein, we have prepared rabbit antiserum against a trpE-HOX-11 fusion protein. The **purified** anti-HOX-11 IgG immunoprecipitated a protein with apparent relative molecular mass of 40 kD. Biochemical fractionation demonstrated that the protein is localized in the nucleus. Furthermore, the HOX-11 **RNA** and protein appeared to be modulated during the cell cycle, with the highest level of expression at G-1/S phase boundary. Taken together, these data suggest that the HOX-11 gene product may function as a transcription factor for G-1 progression in the cell cycle.

2/3,AB/20 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08901830 BIOSIS NO.: 199396053331
Confirmation of Rb gene defects in B-CLL clones and evidence for variable predominance of the Rb defective cells within the CLL clone.

AUTHOR: Kay Neil E(a); Suen Rosa; Ranheim Erik; Peterson Loann C
AUTHOR ADDRESS: (a)P.O. Box 259006, San Diego, CA 92126-9006, USA

JOURNAL: British Journal of Haematology 84 (2):p257-264 1993
ISSN: 0007-1048
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: In 70 B-CLL patients, deletion or **translocation**, at or near the retinoblastoma (Rb) site, was detected in 20 by cytogenetic analysis. **Purified** B cell clones from 13 of these B-CLL patients were isolated and studied for Rb gene status, Rb mRNA and the Rb protein product. Southern blot analysis of the Rb site detected internal deletions (N = 1) or a single allele loss (N = 2) in five patients. Northern blots detected reduced Rb mRNA in four patients. Immunoblot of whole cell lysate revealed reduced levels of unphosphorylated Rb protein in six CLL patients. No CLL B cell clone contained phosphorylated Rb species. These molecular studies have confirmed the cytogenetic alteration of 13q12-14 sites in B-CLL cells. In addition, cytogenetic and molecular biologic analysis suggest heterogeneity in the B cell clone for Rb gene abnormality. B-CLL patients with abnormalities in both cytogenetic and Rb DNA/**RNA** analysis will have a dominance of B cells with an Rb abnormality (N = 5). In patients whose Rb defective CLL cells constitute only a minor subpopulation of the total B cell clone, only cytogenetic defects would likely be detected (N = 7).

2/3,AB/21 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08404565 BIOSIS NO.: 000094122219
DETECTION OF BCR-C-ABL MRNA IN CHRONIC MYELOGENOUS LEUKEMIA BY POLYMERASE CHAIN REACTION TO IDENTIFY **CHROMOSOME TRANSLOCATION**

AUTHOR: LIN C-P; CHEN P-M; YEN J-S; WANG R-L; LEE L-S; CHEN P-H; CHANG J-G
AUTHOR ADDRESS: DEP. CLINICAL PATHOLOGY INTERNAL MED., TAIPEI MUNICIPAL JEN-AI HOSP., NO. 10, SECTION 4, JEN-AI ROAD, TAIPEI, TAIWAN.

JOURNAL: J FORMOSAN MED ASSOC 91 (3). 1992. 247-251.
FULL JOURNAL NAME: Journal of the Formosan Medical Association
CODEN: TIHHA
RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: The hallmark of chronic myelogenous leukemia (CML) is the Philadelphia **chromosome** (Ph1) which is caused by a **translocation** of the c-abl gene from **chromosome** 9 to the breakpoint cluster region (bcr) on **chromosome** 22. Polymerase chain reaction (PCR) can be used to detect the chimeric bcr/c-abl mRNA as evidence of the **translocation**. We applied a very simple and quick method of isolating cytoplasmic **RNA**, as well as reverse transcription and PCR in detecting bcr/c-abl mRNA of seven CML patients in various stages. Our results showed that only a small amount of either peripheral **blood** or **bone marrow** material was required for the expression of the bcr/c-abl mRNA. This is a very fast and time-saving method since a one-step method of cytoplasmic **RNA** isolation is used instead of the several steps in total **RNA**

leukemia and lymphoma have been defined at the molecular level. In addition to advancing understanding of pathological mechanisms underlying the transformation process, the cloning and sequencing of the genes altered by the translocations have provided new tools for diagnosis and monitoring of patients. In particular, the polymerase chain reaction (PCR) methodology yields rapid, sensitive and accurate diagnostic and prognostic information. As leukemias carrying certain translocations confer a higher risk of treatment failure, it is important to identify accurately all positive cases in order to give appropriate therapy. An important new initiative in the diagnostical setting and anti-leukemic therapy is the early detection of minimal residual disease (MRD). If MRD, implying an increased risk of relapse, is reliably detected during apparent clinical remission, alternative strategies could be applied early while the malignant cell burden is still minimal. The PCR assays are clearly more sensitive than other methods of MRD detection including morphology, immunophenotyping and cytogenetics; treatment failure is first detectable by PCR followed by cytogenetic relapse and finally clinical disease. PCR assays have been most often used in the MRD analysis of follicular lymphoma with t(**14**; **18**), chronic myeloid leukemia and acute lymphoblastic leukemia (ALL) with t(**9**;**22**), ALL with t(**4**;**11**), and acute myeloid leukemia (AML) with t(**8**;**21**) or t(**15**;**17**). PCR amplification is applicable to any other translocation provided the translocation is highly associated with the malignancy and the breakpoints are sufficiently clustered; a quickly increasing number of such specific molecular markers are now available for PCR assays. PCR still remains an experimental investigation for the detection of covert disease. However, the clinical relevance of MRD detection should be evaluated separately for each type of leukemia as significant prognostic differences between disease entities were found. This **review** describes the PCR assays available for the detection of leukemia cells with specific **chromosomal translocations** and summarizes the experience with the application of PCR techniques in monitoring patients during the course of the disease.

4/3,AB/12 (Item 12 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08538316 96153138
Tretinoin. A **review** of its pharmacodynamic and pharmacokinetic properties and use in the management of acute promyelocytic leukaemia.
Gillis JC; Goa KL
Adis International Limited, Auckland, New Zealand.
Drugs (NEW ZEALAND) Nov 1995, 50 (5) p897-923, ISSN 0012-6667
Journal Code: EC2
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL
Tretinoin (all-trans retinoic acid), a vitamin A derivative, induces cellular differentiation in several haematological precursor cell lines and cells from patients with acute promyelocytic leukaemia. Drug treatment with tretinoin is associated with morphological and functional maturation of leukaemic promyelocytes and a progressive reduction in the occurrence of the characteristic t(**15**;**17**) **chromosomal translocation%** **%% . Recent therapeutic trials indicate that tretinoin induces remission in 64 to 100% of patients with acute promyelocytic leukaemia. In newly diagnosed patients, remission induction treatment with tretinoin followed by intensive chemotherapy resulted in a significant reduction in relapse rate and prolongation of event-free and overall survival compared with chemotherapy alone in 1 comparative trial. Tretinoin alone does not totally eradicate the leukaemic clone and consolidation chemotherapy is recommended as follow-up. The use of reverse transcription polymerase chain reaction (RT-PCR) provides a sensitive and specific technique to assist in prediction and monitoring of a patient's response to treatment and to help detect the presence of residual or recurrent disease. The use of tretinoin is potentially limited by the rapid and almost universal development of**

0091-7370 Journal Code: 532
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL
Malignancies of childhood include a well-defined spectrum of hematolymphoid, organ specific (adrenal, kidney, liver), soft tissue, bone, and nervous system (central and peripheral) neoplasms with variable biology. Small round cell neoplasms, a subset of childhood malignancies, are histologically similar but differ markedly in their histogenesis, therapy, and prognosis. Traditionally, clinical information and light microscopy, with the aid of histochemistry and ultrastructural evaluation, establish a diagnosis or at least narrow the differential diagnosis. Additionally, immunohistology, cytogenetics, and molecular studies have become important in diagnosis and in defining phenotype/genotype, patient treatment modalities, and prognosis in specific cases. The 11; 22 chromosomal translocation typifies Ewing's sarcoma, primitive neuroectodermal tumor, and Askin's tumor, as does the resultant chimeric transcript, while expression and amplification of N-myc oncogene are predictive of the prognosis in neuroblastoma. Furthermore, studies of genes and gene products are elucidating mechanisms of oncogenesis and tumor progression.

4/3,AB/15 (Item 15 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08197523 95148700
Insights from transgenic mice regarding the role of bcl-2 in normal and neoplastic lymphoid cells.
Cory S; Harris AW; Strasser A
Walter and Eliza Hall Institute of Medical Research, Royal Melbourne Hospital, Victoria, Australia.
Philos Trans R Soc Lond B Biol Sci (ENGLAND) Aug 30 1994, 345 (1313) p289-95, ISSN 0962-8436 Journal Code: P5Z
Contract/Grant No.: CA 43540, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL
The bcl-2 gene was first discovered by molecular analysis of the 14;18 chromosome translocation which is the hallmark of most cases of human follicular lymphoma. To date, it is unique among proto-oncogenes because, rather than promoting cell proliferation, it fosters cell survival. This review summarizes the impact of constitutive bcl-2 expression on the development and function of lymphocytes as well as their malignant transformation. Expression of a bcl-2 transgene in the B lymphoid compartment profoundly perturbed homeostasis and, depending on the genetic background, predisposed to a severe autoimmune disease resembling human systemic lupus erythematosus. T lymphoid cells from bcl-2 transgenic mice were remarkably resistant to diverse cytotoxic agents. Nevertheless, T lymphoid homeostasis was unaffected and tolerance to self was maintained. Expression of high levels of Bcl-2 facilitated the development of B lymphoid tumours but at relatively low frequency and with long latency. Co-expression of myc and bcl-2, on the other hand, promoted the rapid onset of novel tumours which appeared to derive from a lympho-myeloid stem or progenitor cell. Introduction of the bcl-2 transgene into scid mice facilitated the survival and differentiation of pro-B but not pro-T cells, suggesting that a function necessary to supplement or complement the action of Bcl-2 is expressed later in the T than the B lineage. Crosses of the bcl-2 transgenic mice with p53-/- mice have addressed whether loss of p53 function and gain of bcl-2 function are synergistic for lymphoid cell survival.

4/3,AB/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08162893 94207970

Recurrent granulocytic sarcoma. An unusual variation of acute myelogenous leukemia associated with 8;21 chromosomal translocation and blast expression of the neural cell adhesion molecule.

Byrd JC; Weiss RB

Department of Medicine, Walter Reed Army Medical Center, Washington, DC 20307.

Cancer (UNITED STATES) Apr 15 1994, 73 (8) p2107-12, ISSN 0008-543X Journal Code: CLZ

Contract/Grant No.: CA 26806, CA, NCI

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW; REVIEW OF REPORTED CASES

This study reports on a patient with acute myelogenous leukemia (AML) in remission who had a series of 11 granulocytic sarcomas (chloromas or myeloblastomas) appearing periodically over a 29-month interval in a variety of anatomic sites without evidence of bone marrow recurrence. This isolated extramedullary recurrence of AML is distinctly unusual with only 24 cases described previously. This patient had the greatest number and longest reported interval of recurrent granulocytic sarcomas (GS) before bone marrow relapse. Furthermore, he represents the first case of a patient with GS presenting with both an 8;21 chromosomal translocation and neural cell adhesion molecule (CD56) expression. The authors hypothesize that these two abnormalities identified previously as predisposing factors to GS may, in fact, be synergistic for this phenomenon. His case and the review of the literature demonstrate some of the important clinical and management features of a patient who develops GS while in complete marrow remission from previous AML. Although highly sensitive to radiation therapy, the onset of granulocytic sarcomas is almost always followed by bone marrow relapse and should be treated with aggressive reinduction chemotherapy and local irradiation. Such therapy is associated with the longest interval of disease-free survival.

4/3,AB/17 (Item 17 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

07845541 94034752

Somatic point mutations in the translocated bcl-2 genes of non-Hodgkin's lymphomas and lymphocytic leukemias: implications for mechanisms of tumor progression.

Reed JC; Tanaka S

La Jolla Cancer Research Foundation, Cancer Research Center, CA 92037.

Leuk Lymphoma (SWITZERLAND) Jun 1993, 10 (3) p157-63, ISSN 1042-8194 Journal Code: BNQ

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL

The t[14;18] chromosomal translocation is the most common cytogenetic abnormality found in hematolymphoid malignancies. The t[14;18] fuses the bcl-2 gene at 18q21 with the immunoglobulin heavy-chain locus at 14q32, resulting in deregulated expression of bcl-2 and production of high levels of its encoded 26-kD protein in the majority of non-Hodgkin lymphomas. Recent data indicate that somatic point mutations frequently occur in translocated bcl-2 alleles, possibly because of the somatic hypermutation mechanism that is associated with the immunoglobulin gene loci and that normally contributes to antibody diversity. In some cases, these mutations can affect the open reading frame of the bcl-2 gene and thereby alter Bcl-2 proteins. Here, we review the currently available data about the incidence, biological effects, and possible clinical importance of somatic mutations within the translocated bcl-2 genes of human lymphomas and leukemias.

4/3,AB/18 (Item 18 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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06496974 91027590
The 14;18 translocation in European cases of follicular lymphoma: comparison of Southern blotting and the polymerase chain reaction.
Pezzella F; Ralfkiaer E; Gatter KC; Mason DY
Nuffield Department of Pathology, John Radcliffe Hospital, Oxford.
Br J Haematol (ENGLAND) Sep 1990, 76 (1) p58-64, ISSN 0007-1048 Journal Code: AXC
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW OF REPORTED CASES
The 14;18 chromosomal translocation is widely recognized as a cytogenetic abnormality associated with follicular lymphomas, but estimates of its frequency in this type of lymphoma vary widely from less than 50% to almost 90%. Furthermore, no extensive data have been published on the frequency of t(14;18) in European cases of follicular lymphoma. Lymph nodes from 51 patients with follicular lymphomas obtained from two European centres (Oxford and Copenhagen) were examined for the presence of this translocation. Southern blotting and the polymerase chain reaction (PCR) were used in 26 cases and the PCR alone in 25 cases (from which only degraded DNA or formalin fixed samples were available). DNA probes capable of detecting rearrangement at both the major and the minor breakpoint regions were employed. We could detect t(14;18) in only 21 out of 51 cases (41%). However, a review of the literature showed that comparable results have been obtained previously using both cytogenetic and molecular biological techniques and our results support the view that the global incidence of t(14;18) in follicular lymphoma is no greater than 70%. Furthermore, this study has indicated that the PCR is a reliable method for identifying t(14;18) when only formalin-fixed paraffin-embedded tissue or degraded DNA is available.

4/3,AB/19 (Item 19 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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06327378 86027763
Variant Ph translocations in chronic myeloid leukemia.
Heim S; Billstrom R; Kristoffersson U; Mandahl N; Strombeck B; Mitelman F
Cancer Genet Cytogenet (UNITED STATES) Nov 1985, 18 (3) p215-27, ISSN 0165-4608 Journal Code: CMT
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Variant translocations were found in eight of 142 consecutive patients with Ph-positive, chronic myeloid leukemia encountered in our laboratory during the last decade. Two patients had simple, two-way variant translocations: t(17;22)(p13;q11) and t(16;22)(q24;q11). Both of these patients had an additional translocation involving chromosomes #9: t(7;9)(q22;q34) and t(9;17)(q34;q21), respectively. Complex variant translocations were found in four cases: t(2;9;22)(p23q12;q34;q11), t(3;9;22)(p21;q34;q11), t(9;12;22)(q34;q13;q11q13), and t(13;17;22)(p11;p11q21;q11). In two cases, the only discernable cytogenetic aberration was del(22)(q11). A review of the chromosomal breakpoints involved in this series and in 185 cases of variant Ph translocations previously reported in the literature reveals that a disproportionately large number of breakpoints are located in light-staining regions of G-banded chromosomes. Furthermore, the breakpoints in simple variant translocations are more often located in terminal chromosomal regions, whereas, the breakpoints in complex translocations typically affect nonterminal bands. No obvious correlation

was detected [redacted] fragile sites, [redacted]cogene locations, or consisten[redacted]hromosome breakpoints in other malignancies.

4/3,AB/20 (Item 20 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05158669 88105821
Familial Miller-Dieker syndrome and (15;17) chromosome translocation]
Syndrome de Miller-Dieker familial et translocation chromosomique (15;17).
Goutieres F; Aicardi J; Rethore MO; Prieur M; Lejeune J
Unite de Neurologie Infantile, Hopital des Enfants-Malades, Paris.
Arch Fr Pediatr (FRANCE) Aug-Sep 1987, 44 (7) p501-4, ISSN 0003-9764 Journal Code: 71Q
Languages: FRENCH Summary Languages: ENGLISH
Document type: JOURNAL ARTICLE English Abstract
Two siblings with familial lissencephaly presented with the clinical and neuropathological features of the Miller-Dieker syndrome. High resolution caryotype demonstrated a 46,XX,-17+der(17)t(15;17)pat translocation with partial deletion of the short arm of chromosome 17 in one patient and a balanced 46,XY,t(15;17)(q2600;p1300) translocation in the father. Review of the literature uncovered 14 additional patients with Miller-Dieker syndrome and partial deletion of the short arm of chromosome 17. A cytogenetic study should be done in all cases of lissencephaly for genetic counselling.

4/3,AB/21 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11700517 BIOSIS NO.: 199800482248
Clinical, pathologic, and molecular spectrum of tumors associated with t(11;22)(p13;q12): Desmoplastic small round-cell tumor and its variants.

AUTHOR: Gerald William L(a); Ladanyi Marc; De Alava Enrique; Cuatrecasas Miriam; Kushner Brian H; Laquaglia Michael P; Rosai Juan
AUTHOR ADDRESS: (a)Dep. Pathol., Memorial Sloan-Kettering Cancer Cent., 1275 York Ave., New York, NY 10021, USA

JOURNAL: Journal of Clinical Oncology 16 (9):p3028-3036 Sept., 1998
ISSN: 0732-183X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Purpose: Intense investigation has reshaped concepts about undifferentiated tumors occurring in young people (small round-cell tumors). Tumors associated with t(11;22)(p13;q12) and descriptively designated desmoplastic small round-cell tumor (DSRCT) are a distinctive, rare, poorly understood member of this family. We reviewed 109 cases of DSRCT to further characterize this entity better. Methods: Clinical information and histology were reviewed. Immunohistochemistry and immunoblotting were performed using standard techniques. Chimeric EWS-WT1 RNA and DNA were detected by polymerase chain reaction (PCR) and genomic translocation breakpoints mapped in a subset of cases. Results: There were 90 males and 19 females from 6 to 49 years of age (mean, 22 years). A total of 103 had tumor in the abdominal cavity, four in the thoracic region, one in the posterior cranial fossa, and one in the hand. Typical histologic and immunohistochemical features were usually evident

components, cytology, architecture, and immunoreactivity occurred. Tumor cells were usually reactive with antibodies to keratin (67 of 78 cases, 86%), epithelial membrane antigen (50 of 54, 93%), vimentin (64 of 66,97%), desmin (70 of 78,90%), neuron-specific enolase (60 of 74, 81%), and the EWS-WT1 chimeric protein (25 of 27,93%); typically nonreactive for muscle common actin (one of 58, 2%), myogenin (zero of eight, 0%), and chromogranin (one of 46, 2%); and variably reactive for MIC2 (nine of 47, 20%) and p53 (five of 17 with > 20% tumor cells reactive). Functional EWS-WT1 gene fusion was evident in 25 of 26 cases with genomic breakpoints in WT1 intron 7, and EWS introns 7, 8, and 9. Prognosis in general is poor, but tumors are responsive to aggressive therapy. Conclusion: This large review identifies a greater degree of clinical, pathologic, and molecular variation than originally appreciated for tumors associated with t(11;22)(p13;q12). Translocation and functional fusion of the EWS and WT1 genes appears to be a consistent feature of this unique tumor.

4/3,AB/22 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11298487 BIOSIS NO.: 199800079819
Polymerase chain reaction amplification of long DNA targets: Application to analysis of chromosomal translocations in human B-cell tumors (Review).

AUTHOR: Akasaka Takashi; Akasaka Hiroshi; Ohno Hitoshi(a)
AUTHOR ADDRESS: (a)First Div., Dep. Internal Med., Fac. Med., Kyoto Univ., 54-Shogoin-Kawaramachi, Sakyo-ku, Kyoto , Japan

JOURNAL: International Journal of Oncology 12 (1):p113-121 Jan., 1998
ISSN: 1019-6439
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Chromosomal translocations in human leukemias generate fusion transcripts containing messages from two genes involved in the translocation, and these have been the targets for reverse transcriptase-mediated polymerase chain reaction (PCR). In contrast, many of the translocations in B-cell tumors involve immunoglobulin gene (IG) loci, and coding regions of the oncogenes on partner chromosomes are not interrupted by the translocation. Therefore, targets for PCR amplification are single-copy oncogene/IG fusion sequences within the complex genomic DNA. We present here a novel strategy for detection of translocations in B-cell tumors on the basis of long-distance (LD-) PCR that is capable of amplifying up to 30 kb of DNA. LD-PCR is a general method using primer pairs designed for distinctive regions of IG and oncogenes involved in translocations, and amplifying long DNA fragments encompassing the oncogene/IG junction. LDPCR is capable of detecting virtually all the important translocations in B-cell tumors, including, t(8;14)(q24;q32), t(14;18)(q32;q21), t(3;14)(q27;q32) and its variants. We show here that LD-PCR can substitute for time-consuming, Southern blot hybridization in the rapid detection of these translocations. Furthermore, as amplified fragments obtained by LD-PCR contained exons and flanking sequences of the oncogenes and IGs, restriction analysis and nucleotide sequencing of the products refined the characteristics of translocations.

4/3,AB/23 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10516768 BIOSIS NO.: 199699137913
A long way from definition of the molecular basis to benefit in the clinical management of Ewing tumours.

AUTHOR: Kovar H(a); Zoubek A; Gadner H
AUTHOR ADDRESS: (a)Children's Cancer Res. Inst., St. Anna Kinderspital, Kinderspitalgasse 6, A-1090 Vienna, Austria

JOURNAL: Onkologie 19 (3):p234-240 1996
ISSN: 0378-584X
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English; German

ABSTRACT: Recently, the Ewing family of turnouts (ET), previously classified by clinical appearance and histology as Ewing's sarcoma (ES), Askin turnout, peripheral primitive neuroectodermal turnout (pPNET) or neuroepithelioma, has been redefined on a purely molecular basis - the presence of specific gene rearrangements. Here, we describe how the recent genetic findings have influenced our view of ET pathophysiology. The t(11;22), t(21;22), t(7;22) and t(17;22) chromosomal translocations fuse the EWS gene to members of the ETS oncogene family. We present a new functional model for the generation of ET that might explain variable neural marker expression in an otherwise non-neural crest-derived cell by unscheduled gene activation. Currently, two thirds of patients with non-metastatic disease can be cured by multimodal therapy. Patients presenting with metastases, however, have an adverse prognosis which is increasingly combatted by myeloablative therapy. Molecular detectability of ET specific aberrations has stimulated great hopes as to the definition of high-risk patients by PCR screening for tumor cells in blood, bone marrow and stem cell phereses. Positive results have been obtained as a consequence of metastatic tumour spread but also due to a large turnout burden or to traumatic or surgical tumour cell mobilisation. Physiological and sampling parameters influence the outcome of the analysis. Thus, the significance of negative/positive results for minimal residual and metastatic disease detection remains to be established. Dissection of the functional cascade in which the aberrant ETS transcription factor is involved might aid in identifying novel biological treatment modalities for the high-risk group of patients. The scope of this review is to describe the potential input of molecular biology on the clinical management of ET as a model tumour and should separate realistic perspectives from utopic dreams.

4/3,AB/24 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09670200 BIOSIS NO.: 199598125118
Changing trends in the management of chronic granulocytic leukemia.

AUTHOR: Tefferi Ayalew
AUTHOR ADDRESS: Mayo Clinic, 200 First St. SW, Rochester, MN 55905, USA

JOURNAL: International Journal of Oncology 6 (1):p163-166 1995
ISSN: 1019-6439
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Current evidence strongly implicates the chromosome translocation t(9;22) as the cause of chronic

granulocytic leukemia (CGL). Therefore, the identification of the genetic aberrancy through either cytogenetic or molecular methods is a requirement for diagnosis. Furthermore, qualitative and quantitative methods of detecting t(9;22) are useful in monitoring response status and disease progression. Advances have been made in the management of the disease in its chronic phase, but the blast phase of CGL remains terminal. In this review, the available treatment options in chronic-phase CGL are discussed.

4/3,AB/25 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09436135 BIOSIS NO.: 199497444505
Standard polymerase chain reaction analysis does not detect t(14; 18) in reactive lymphoid hyperplasia.

AUTHOR: Segal Glenn H(a); Scott Marda; Jorgensen Trevor; Braylan Raul C
AUTHOR ADDRESS: (a)Hematopathol. Sect., Dep. Pathol. and Lab. Med., Univ. Florida Coll. Med., Box 100275, JHMHC, Ga, USA

JOURNAL: Archives of Pathology and Laboratory Medicine 118 (8):p791-794 1994
ISSN: 0363-0153
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: There are conflicting data regarding the detection of t(14; 18) in reactive lymphoid hyperplasia (RLH) by the polymerase chain reaction (PCR). Although most studies have not detected t(14; 18), several groups have definitively shown that a very low number of cells with this translocation (one in 10-5 to 10-6) are present in a significant proportion of follicular hyperplasias. Review of the methods from these series reveals that modifications of the PCR assay (i.e., enhanced sensitivity steps such as seminesting, lengthy autoradiographic exposure times, multiple aliquot reactions of single samples, and/or high concentrations of template DNA) are probably necessary to detect t(14;18) in RLH. We evaluated a diverse set of 111 RLH (85 lymph nodes, 22 tonsils, and four other sites) from patients of different age groups (age range, 9 months to 80 years) to determine if a standard PCR assay would amplify t(14;18). Of these, 61 (55%) specimens had a prominent follicular hyperplastic component. Fifty-seven follicular lymphomas served as a control group. Polymerase chain reaction was performed as a single-run, two-primer-based assay for major breakpoint region bcl-2 translocations (5' major breakpoint region primer and 3' immunoglobulin heavy-chain gene-joining region consensus primer). Two different types of thermocyclers were employed. A metal block thermocycler was used with 35 cycles of amplification on 500 ng to 1 mu-g of genomic DNA, and a separate air thermocycler was used with 45 cycles of amplification on 50 ng of genomic DNA. Product detection was carried out through ethidium bromide staining and UV gel illumination, along with a digoxigenin-alkaline phosphatase-based, internal major breakpoint region oligonucleotide probe system. We found no amplified t(14;18) products in any RLH. In contrast, 36 (63%) of 57 follicular lymphomas showed t(14; 18) (published range for detection of major breakpoint region translocations by PCR, 31% to 74%). Moreover, the assay's sensitivity, estimated through dilution studies, was to one in 10-4 to 10-5 cells. Although theoretically possible, our data suggest that there is practically no risk of amplifying a t(14;18) from RLH when utilizing a standard PCR assay.

4/3,AB/26 (Item 6 from file: 5)
DIALOG(R)File [redacted] Biosis Previews(R)

07820400 BIOSIS NO.: 000092101586
INVOLVEMENT OF THE BCL2 GENE IN 131 CASES OF NON-HODGKIN'S B LYMPHOMAS ANALYSIS OF CORRELATIONS WITH IMMUNOLOGICAL FINDINGS AND CELL CYCLE

AUTHOR: CORNILLET P; RIMOKH R; BERGER F; FFRENCH M; ROUAULT J-P; WAHBI K; BRYON P-A; GENTILHOMME O; COIFFIER B; ET AL
AUTHOR ADDRESS: LAB. CENTRAL D'HEMATOLOGIE CYTOGENETIQUE, PAVILLON E, HOPITAL EDOUARD HERRIOT, PLACE D'ARSONVAL, 69437 LYON CEDEX, FR.

JOURNAL: LEUK LYMPHOMA 4 (5-6). 1991. 355-362.
CODEN: LELYE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The t(14;18) chromosomal translocation is widely recognized as a cytogenetic abnormality associated with follicular lymphomas, but estimates of its frequency in this type of lymphoma vary from less than 40% to almost 90% according to the geographic origin of the patients. Using two human genomic probes for major and minor breakpoint cluster regions mapping at chromosome 18q21, we have analysed 131 cases of B non-Hodgkin's lymphomas obtained from France, by the Southern blot technique. The genotypic study was complemented in most cases by immunophenotypic and cell kinetic analyses. The BCL2 gene located at 18wq21 band was rearranged in 39 of 56 (70%) follicular lymphomas and in 9 of 74 (12%) diffuse lymphomas; probes for major and minor breakpoint regions detected two thirds and one third of the rearrangements respectively. Regarding the morphologic subtypes of follicular and diffuse lymphomas, no significant differences were observed irrespective of the probe used. Review of the literature showed that comparable results have been obtained previously using both cytogenetic and molecular approaches and our results support the view that the global incidence of the t(14;18)(q32;q21) translocation in follicular lymphomas is about 70% with wide geographic variations. The immunological study provides evidence for a significant correlation of BCL2 rearrangement with surface immunoglobulin gamma isotype expression and with the lack of reactivity of the malignant cells with an antibody against the CD5 cluster. In the cases where cell kinetics was analysed, we did not find any significant difference between the rate of proliferation and BCL2 rearrangement. These data should be compared with previously reported observations made in humans or in transgenic mice and enable us to propose a model accounting for the role of BCL2 in B cell tumorigenesis.

4/3,AB/27 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05086421 BIOSIS NO.: 000081044545
VARIANT PHILADELPHIA CHROMOSOMES TRANSLOCATIONS IN CHRONIC MYELOID LEUKEMIA

AUTHOR: HEIM S; BILLSTROM R; KRISTOFFERSSON U; MANDAHL N; STROMBECK B; MITELMAN F
AUTHOR ADDRESS: DEP. CLINICAL GENETICS, UNIV. HOSPITAL, S-221 85 LUND, SWEDEN.

JOURNAL: CANCER GENET CYTOGENET 18 (3). 1985. 215-228.
FULL JOURNAL NAME: Cancer Genetics and Cytogenetics
CODEN: CGCYD
RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Variant translocations were found in eight of 142 consecutive patients with Ph-positive, chronic myeloid leukemia encountered in our laboratory during the last decade. Two patients had simple, two-way variant translocations: t(17;22)(p13;q11) and t(16;22)(q24;q11). Both of these patients had an additional translocation involving chromosome #9; t(7;9)(q22;q34) and t(9;17)(q34;q21), respectively. Complex variant translocations were found in four cases: t(2;9;22)(p23q12;q34;q11), t(3;9;22)(p21;q34;q11), t(9;12;22)(q34;p13;q11q13), and t(13;17;22)(p11;p11q21;q11). In two cases, the only discernable cytogenetic aberration was del(22)(q11). A review of the chromosomal breakpoints involved in this series and in 185 cases of variant Ph translocations previously reported in the literature reveals that a disproportionately large number of breakpoints are located in light-staining regions of G-banded chromosomes. Furthermore, the breakpoints in simple variant translocations are more often located in terminal chromosomal regions, whereas, the breakpoints in complex translocations typically affect nonterminal bands. No obvious correlation was detected between variant pH translocation breakpoints and either fragile sites, oncogene locations, or consistent chromosome breakpoints in other malignancies.

4/3,AB/28 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

03949442 BIOSIS NO.: 000076035008
VARIANT PHILADELPHIA CHROMOSOME TRANSLOCATIONS IN CHRONIC MYELOGENOUS LEUKEMIA AND THEIR INCIDENCE INCLUDING 2 CASES WITH SEQUENTIAL LYMPHOID AND MYELOID CRISES

AUTHOR: OSHIMURA M; OHYASHIKI K; TERADA H; TAKAKU F; TONOMURA A
AUTHOR ADDRESS: DEP. CYTOGENETICS, MED. RES. INST., TOKYO MED. DENT. UNIV., TOKYO 113, JPN.

JOURNAL: CANCER GENET CYTOGENET 5 (3). 1982. 187-202.
FULL JOURNAL NAME: Cancer Genetics and Cytogenetics
CODEN: CGCYD
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A serial cytogenetic study of 110 cases of chronic myelogenous leukemia (CML) was performed with G- and/or Q-banding techniques with the following results. Seven out of the 110 cases were karyotypically normal. A variant Ph1 translocation was observed in 3 cases. In 1 case, the leukemic cells contained 2 reciprocal translocations, i.e., a t(3;9)(q21;q34) and a t(17;22)(q21;q11); therefore, a Ph1 chromosome was masked by a translocation of the deleted material from the 17q onto the band q11 of the long arm of chromosome 22. In the 2nd case, a variant Ph1 translocation involved chromosomes 9, 20 and 22, resulting in a karyotype interpreted as 46,XX,t(9q+;20q+;22q-); in this rearrangement, one of the segments, i.e., 9q31 or 9q33, seemed to be interstitially deleted and inserted into the interstitial region (q11) of a chromosome 20 and the 22q11 .fwdarw. qter was translocated onto the 9q. This is the 1st case in which chromosome 20 was involved in a variant Ph1 translocation. In the 3rd case, the karyotype of leukemic cells was interpreted as 46,XY,t(5;9;22)(q13;q34;q11). The frequency of Ph1-negative CML [chronic myelogenous leukemia] and that of Ph1-positive CML with various types of Ph1 translocation from 15 studies reported as series of 25 or more cases, including the present study, were tabulated. The incidence of a variant Ph1 translocation was 4.1% (42/1027 cases of Ph1-positive CML); of the 42, 13 were of a simple type and 29 of a complex type. A masked Ph1 by a translocation of material onto the short arm of the 22q- was

4/3,AB/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09188577 97379050
The AML1 gene: a transcription factor involved in the pathogenesis of myeloid and lymphoid leukemias.
Lo Coco F; Pisegna S; Diverio D
Department of Human Biopathology, University La Sapienza of Rome, Italy. lococo@dbu.uniroma1.it
Haematologica (ITALY) May-Jun 1997, 82 (3) p364-70, ISSN 0390-6078
Journal Code: FYB
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL
BACKGROUND AND OBJECTIVE: The AML1 gene was identified in 1991 by cloning the t(**8;21**) **chromosome translocation** associated with FAB M2 acute myeloid leukemia (AML). AML1 encodes a nuclear transcription factor (TF) which shows homology in its 5' part with the Drosophila melanogaster segmentation gene, runt, and contains a transactivation domain in the carboxyterminal portion. In the t(**8;21**), AML1 is fused to the ETO (MTG8) gene, resulting in a hybrid AML1/ETO mRNA, which in turn is translated into a chimeric protein. The objective of this article is to **review** here the main structural and biological features of AML1 and of its fusion products, with special focus on their clinical correlations and their potential usefulness for prognostic and monitoring studies in **human** leukemia. EVIDENCE AND INFORMATION SOURCES: The material examined in the present **review** includes articles and abstracts published in journals covered by the Science Citation Index and Medline. STATE OF ART: The normal AML-1 protein forms the alpha-subunit of the heterodimeric TF core binding factor (or CBF), whose beta-subunit is encoded by the CBF beta gene on chromosome 16q22. CBF beta is rearranged and fused to the MYH11 gene in the AML M4Eo-associated inv(16) aberration. Thus, the two most common chromosome abnormalities of AML, i.e. t(**8;21**) and inv(16), affect the two subunits of the same target protein. This suggests that the wild type CBF must exert an important role in the control of myeloid cell growth and/or differentiation. Evidence that AML1 is a pivotal regulator of definitive hematopoiesis has been recently provided by analyzing AML1 knockout mice. The chromosome region 21q22, where AML1 maps, is involved in several other karyotypic aberrations, such as the t(3;21) translocation associated with a subset of therapy-related myelodysplastic syndromes and AML, and the blast phase of chronic myelogenous leukemia. In this abnormality, three distinct genes: EVI1, EAP, MDS1, located on chromosome band 3q26, have been identified that may recombine with AML1. Finally, the recently cloned t(**12;21**) translocation has been found to involve the TEL gene (coding for a novel TF) on 12p13, and AML1 on 21q22. This alteration, which results in the production of a TEL/AML1 chimeric protein, is restricted to pediatric B-lineage acute lymphoid leukemia (ALL), where it represents the most frequent molecular defect known to date (up to 25% of cases). Strikingly, the same t(**12;21**) is identified in only 0.05% of pediatric B-lineage ALL cases analyzed by conventional karyotyping. Other relevant characteristics of TEL/AML1-positive ALL are frequent deletion of the other TEL allele and association with an excellent prognostic outcome. PERSPECTIVES: It is expected that future studies will provide more detailed information on the leukemogenic effect of AML1 alterations, and better define the prognostic relevance of detecting the hybrid proteins formed by this gene at diagnosis and during remission.

4/3,AB/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

insights and approaches to the classification of tumors with [illegible] prognostic and therapeutic implications. We review the potentially diagnostic immunohistochemical and molecular markers of soft tissue tumors (STTs). The immunohistochemical markers reviewed include vimentin, cytokeratin, desmin, HHF35, S100, myoD1, alphal-antitrypsin, vascular markers (factor VIII, CD31, CD34), MIC2, and others. The potentially diagnostic **chromosomal translocations** and associated genes identified in STT include Ewing's/PNET t(**11;22**)(q24;q12)(FLI1;EWS), t(21;22)(q22;q12)(ERG; EWS); t(7;22)(p22;q12)(ETV1;EWS); desmoplastic small round cell tumor t(**11;22**)(p13;q12)(WT1;EWS); extraskeletal myxoid chondrosarcoma t(**9;22**)(q22;q12) (TEC(CHN);EWS); malignant ectomesenchymoma t(**11;22**)(q24;q12)(FLI1;EWS); alveolar rhabdomyosarcoma t(**2;13**)(q35;q14)(PAX-3;FKHR); t(1;13) (p36;q14)(PAX-7;FKHR); myxoid and round cell liposarcoma t(12;16)(q13;p11)(CHOP;TLS(FUS)); synovial sarcoma t(X;18)(p11;q11)(SSX1&2;SYT), and others. The nature, utility, and limitations of these markers in diagnostic settings are explored.

4/3,AB/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09220417 97438992
Assessment of molecular genetic detection of **chromosome translocations** in the differential diagnosis of pediatric sarcomas.
Dockhorn-Dworniczak B; Schafer KL; Blasius S; Christiansen H; Koscielniak E; Ritter J; Winkelmann W; Jurgens H; Bocker W
Gerhard-Domagk-Institut fur Pathologie, Munster.
Klin Padiatr (GERMANY) Jul-Aug 1997, 209 (4) p156-64, ISSN 0300-8630
Journal Code: KWE
Languages: ENGLISH
Document type: JOURNAL ARTICLE
BACKGROUND: Recent studies have shown that many types of soft-tissue sarcomas are characterized by specific **chromosomal translocations**, which are likely to be of etiologic significance. In order to evaluate their diagnostic impact, a panel of 129 sarcomas comprising 78 Ewing's tumors (ET), 19 rhabdomyosarcomas (RMS), 20 neuroblastomas (NB), 9 synovialsarcomas, 2 esthesioneuroblastomas, and 1 desmoplastic small-round-cell tumor (DSRCT) were analysed for the occurrence of the major recurrent translocations, such as t(**11;22**)(q24;q12), t(21;22)(q22;q12), t(**11;22**)(p13;q12), t(**2;13**)(q35;q14), t(1;13)(p36;q14), and t(X;18)(p11;q11). METHODS: Nitrogen-frozen tissue material was analysed by means of Reverse Transcription followed by PCR (Polymerase-Chain Reaction) and nested PCR (RT-PCR). Specificity of the PCR products obtained was confirmed by non-isotopic Southern-Blot analysis with gene-specific probes and/or automated direct sequence analysis. RESULTS: 75 ETs have been shown to carry either a t(**11;22**) or t(21;22) translocation by identification of chimeric EWS-FLI-1 or EWS-ERG gene-fusion transcripts respectively. 3 ETs were lacking EWS/FLI-1 or EWS-ERG fusion products. 2 of these tumors were shown on **review** to have unusual morphological features for ETs. 8/19 RMS were initially diagnosed as alveolar RMS. These tumours were shown to carry either a t(**2;13**) translocation exhibiting chimeric PAX3-FKHR fusion transcripts or a t(1;13) translocation with PAX7-FKHR chimeric gene products. One RMS of the embryonal group also carried a t(1;13) translocation. Reevaluation demonstrated a partly alveolar morphology. In 8/9 synovial sarcomas a t(X;18) translocation was identified. Expression of a EWS-WTI gene-fusion product associated with a t(**11;22**) translocation was found in the DSRCT. None of these rearrangements were detected in the NBs and 2 esthesioneuroblastomas. CONCLUSIONS: Our results support the concept that the major recurrent translocations are histogenetically specific for a subset of sarcomas. Thus, the detection of tumor type-specific translocations represents an extremely useful diagnostic modality as an adjunct to surgical pathology.

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        560959  RNA
       2609898  BLOOD
        516267  BONE
        217082  MARROW
        203897  BONE(W)MARROW
        739329  PLASMA
        391397  CHROMOSOM?
         91812  TRANSLOCAT?
        771076  PURIF?
     S1     21  RNA AND (BLOOD OR BONE (W) MARROW OR PLASMA) AND
                CHROMOSOM? AND TRANSLOCAT? AND PURIF?

? rd

...completed examining records
     S2     21  RD (unique items)
? t s2/3,ab/all


 2/3,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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09211286   97449106
  BCR/ABL-negative progenitors are enriched in the adherent fraction of
CD34+ cells circulating in the blood of chronic phase chronic myeloid
leukemia patients.
  Grand FH; Marley SB; Chase A; Titley I; Healy L; Spencer A; Reiter A;
Goldman JM; Gordon MY
  Leukemaemia Research Fund Centre for Adult Leukaemia, Royal Postgraduate
Medical School, London, UK.
  Leukemia (ENGLAND) Sep 1997, 11 (9) p1486-92, ISSN 0887-6924
Journal Code: LEU
  Languages: ENGLISH
  Document type: JOURNAL ARTICLE
  Philadelphia chromosome -positive (Ph+) hemopoietic cells
predominate in patients with chronic myeloid leukemia (CML) in chronic
phase, but some Ph presumably normal stem cells persist in most patients.
Ph cells are relatively frequent, compared to mature cell populations, in
primitive hemopoietic cell populations from CML patients. We have
purified CD34+ cells from chronic phase CML blood and separated
them into two fractions on the basis of adherence or non-adherence to
tissue culture plastic. We also separated CD34+ CML cell populations into
HLA-DR(hi) and HLA-DR(lo) fractions and CD38(hi) and CD38(lo) fractions by
flow cytometry. The CD34+ cells that adhered to plastic were predominantly
CD33-, CD38- and HLA(-)-DR; cells with these phenotypic properties were
significantly rarer in the CD34+ non-adherent cell population (P =
0.008-0.02). Expression of p210 BCR/ABL mRNA by adherent, non-adherent,
HLA-DR(hi) and HLA-DR(lo)CD34+ cell subpopulations was demonstrated by
RT-PCR. Using fluorescence in situ hybridization (FISH) in conjunction with
BCR and ABL probes we detected Ph+ and Ph- cells in both adherent and
non-adherent CD34+ cell fractions of 15/15 patients studied and in the
HLA-DR(lo) or CD38(lo) sorted CD34+ cell fractions. The concentration of
Ph- cells in the adherent CD34+ cell fraction was three-fold higher than in
the non-adherent fraction (P = 0.001). Ph- adherent cells were detected in
untreated CML patients and as late as 6 years after diagnosis of CML in
patients treated with hydroxyurea (HU) or interferon-alpha (IFN-alpha). We
conclude that whilst appreciable numbers of Ph- primitive hemopoietic
progenitors are present in the circulation in untreated patients and also
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in treated patients in late chronic phase, the majority of cells expressing CD34 but not CD[redacted] CD38 or HLA-DR antigens, are [redacted]t of the CML clone.

2/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09083673 97303198
BCL8, a novel gene involved in **translocations** affecting band 15q11-13 in diffuse large-cell lymphoma.
Dyomin VG; Rao PH; Dalla-Favera R; Chaganti RSK
Cell Biology Program and the Department of Human Genetics, Memorial Sloan-Kettering Cancer Center, 1275 York Avenue, New York, NY 10021, USA.
Proc Natl Acad Sci U S A (UNITED STATES) May 27 1997, 94 (11) p5728-32
, ISSN 0027-8424 Journal Code: PV3
Contract/Grant No.: CA-34775, CA, NCI; CA-66999, CA, NCI; CA-44029, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Translocations affecting the **chromosomal** region 15q11-13 and various other partners are recurrent in diffuse large-cell lymphomas (DLCL). To identify the putative gene, here named BCL8, involved in these **translocations** we have cloned the breakpoint region from a DLCL patient with t(14;15)(q32;q11-13) and the corresponding germ-line region from **chromosome** 15. The genomic locus on **chromosome** 15 is clonally rearranged in about 4% of DLCL in agreement with the frequency of 15q11-13 **translocations**. A probe derived from the BCL8 locus on **chromosome** 15 detected a transcript in human testis and prostate, whereas no expression was found in spleen, thymus, and **blood** leukocytes. Analysis of the BCL8 cDNA clones isolated from human testis cDNA library showed that the BCL8 gene generates a major transcript of 2.6 kb and a less prominent 4.5-kb species due to differential polyadenylylation. By reverse transcription-PCR analysis of **RNA** extracted from frozen DLCL samples and lymphoma cell lines, BCL8 expression was detected in all patients carrying 15q11-13 abnormalities and in a fraction of randomly selected DLCL patients. These results suggest that the BCL8 gene is not normally expressed in lymphoid tissues, but its expression can be activated by **chromosomal translocation** or by other mechanisms in DLCL. Ectopic expression of BCL8 in a significant proportion of DLCL suggests an important role for this gene in the molecular pathogenesis of B cell lymphoma.

2/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08869198 97083580
The CBFbeta subunit is essential for CBFalpha2 (AML1) function in vivo.
Wang Q; Stacy T; Miller JD; Lewis AF; Gu TL; Huang X; Bushweller JH; Bories JC; Alt FW; Ryan G; Liu PP; Wynshaw-Boris A; Binder M; Marin-Padilla M; Sharpe AH; Speck NA
Department of Biochemistry, Dartmouth Medical School, Hanover, New Hampshire 03755, USA.
Cell (UNITED STATES) Nov 15 1996, 87 (4) p697-708, ISSN 0092-8674
Journal Code: CQ4
Contract/Grant No.: NS22897, NS, NINDS; AI39536-01, AI, NIAID; CA58343, CA, NCI; +
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The CBFbeta subunit is the non-DNA-binding subunit of the heterodimeric core-binding factor (CBF). CBFbeta associates with DNA-binding CBFalpha subunits and increases their affinity for DNA. Genes encoding the CBFbeta subunit (CBFB) and one of the CBFalpha subunits (CBFA2, otherwise known as

The t(16;21)(p11;q22) **translocation** is a nonrandom **chromosomal** abnormality found in several types of myeloid leukemia, which show variable cytomorphological features. We constructed rodent-human somatic cell hybrids containing the der(16) **chromosome** from leukemic cells of a patient with t(16;21). Using these hybrids, we mapped the **translocation** breakpoint on the Not I restriction map of **chromosome** 21 which we had previously constructed. The result showed the proximity of the breakpoint to the ERG gene, a member of the ets oncogene superfamily. Polymerase chain reaction and Southern blot analyses of genomic DNA from the hybrids and from peripheral **blood** cells and **bone marrow** cells of patients with t(16;21) showed that the breakpoints were clustered within a single intron in the coding region of the ERG gene. This finding and the results obtained by Northern blot analysis suggested the formation of a chimeric product(s) by fusion of the ERG gene and an unknown counterpart gene on **chromosome** 16.

2/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07810886 93132070
A family of cation ATPase-like molecules from Plasmodium falciparum.
Krishna S; Cowan G; Meade JC; Wells RA; Stringer JR; Robson KJ
Medical Research Council Molecular Haematology Unit, John Radcliffe Hospital, Oxford, United Kingdom.
J Cell Biol (UNITED STATES) Jan 1993, 120 (2) p385-98, ISSN 0021-9525
Journal Code: HMV
Languages: ENGLISH
Document type: JOURNAL ARTICLE
We report the nucleotide and derived amino acid sequence of the ATPase 1 gene from Plasmodium falciparum. The amino acid sequence shares homology with the family of "P"-type cation **translocating** ATPases in conserved regions important for nucleotide binding, conformational change, or phosphorylation. The gene, which is present on **chromosome** 5, has a product longer than any other reported for a P-type ATPase. Interstrain analysis from 12 parasite isolates by the polymerase chain reaction reveals that a 330-bp nucleotide sequence encoding three cytoplasmic regions conserved in cation ATPases (regions a-c) is of constant length. By contrast, another 360-bp sequence which is one of four regions we refer to as "inserts" contains arrays of tandem repeats which show length variation between different parasite isolates. Polymorphism results from differences in the number and types of repeat motif contained in this insert. Inserts are divergent in sequence from other P-type ATPases and share features in common with many malarial antigens. Studies using **RNA** from the erythrocytic stages of the malarial life cycle suggest that ATPase 1 (including the sequence which encodes tandem repeats) is expressed at the large ring stage of development. Immunolocalization has identified ATPase 1 to be in the region of the parasite **plasma** membrane and pigment body. These findings suggest a possible model for the genesis of malarial antigens.

2/3,AB/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07363269 92224879
Genomic variability and alternative splicing generate multiple PML/RAR alpha transcripts that encode aberrant PML proteins and PML/RAR alpha isoforms in acute promyelocytic leukaemia.
Pandolfi PP; Alcalay M; Fagioli M; Zangrilli D; Mencarelli A; Diverio D; Biondi A; Lo Coco F; Rambaldi A; Grignani F; et al
Istituto Clinica Medica I, University of Perugia, Italy.
EMBO J (ENGLAND) Apr 1992, 11 (4) p1397-407, ISSN 0261-4189

Journal Code: EMB
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The acute promyelocytic leukaemia (APL) 15;17 **translocation** generates a PML/RAR alpha chimeric gene which is transcribed as a fusion PML/RAR alpha mRNA. Molecular studies on a large series of APLs revealed great heterogeneity of the PML/RAR alpha transcripts due to: (i) variable breaking of **chromosome** 15 within three PML breakpoint cluster regions (bcr1, bcr2 and bcr3), (ii) alternative splicings of the PML portion and (iii) alternative usage of two RAR alpha polyadenylation sites. Nucleotide sequence analysis predicted two types of proteins: multiple PML/RAR alpha and aberrant PML. The PML/RAR alpha proteins varied among bcr1, 2 and 3 APL cases and within single cases. The fusion proteins contained variable portions of the PML N terminus joined to the B-F RAR alpha domains; the only PML region retained was the putative DNA binding domain. The aberrant PML proteins lacked the C terminus, which had been replaced by from two to ten amino acid residues from the RAR alpha sequence. Multiple PML/RAR alpha isoforms and aberrant PML proteins were found to coexist in all APLs. These findings indicate that two potential oncogenic proteins are generated by the t(15;17) and suggest that the PML activation pathway is altered in APLs.

2/3,AB/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07363058 92217981
Beta satellite DNA: characterization and localization of two subfamilies from the distal and proximal short arms of the human acrocentric **chromosomes**.
Greig GM; Willard HF
Department of Genetics, Stanford University, California 94305.
Genomics (UNITED STATES) Mar 1992, 12 (3) p573-80, ISSN 0888-7543
Journal Code: GEN
Contract/Grant No.: HG00107, HG, NHGRI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
beta satellite is a repetitive DNA family that consists of approximately 68-bp monomers tandemly repeated in arrays of at least several hundred kilobases. In this report we describe and characterize two subfamilies located exclusively on the human acrocentric **chromosomes**. The first subfamily is defined by a homogeneous approximately 2.0-kb higher-order repeat unit and is located primarily distal to the ribosomal **RNA** gene cluster, based both on fluorescence in situ hybridization to metaphase **chromosomes** and on filter hybridization analysis of **translocation chromosomes** isolated in somatic cell hybrids. In contrast, the second subfamily is located both distal and proximal to the ribosomal **RNA** gene cluster on the same acrocentric **chromosomes**. The DNA sequences of a number of monomers from these two subfamilies are compared to each other and to other beta satellite monomers to assess both inter- and intrasubfamily sequence relationships for these monomers.

2/3,AB/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07323725 92236602
Altered **chromosome** 6 in immortal human fibroblasts.
Hubbard-Smith K; Patsalis P; Pardinas JR; Jha KK; Henderson AS; Ozer HL
Department of Microbiology and Molecular Genetics, UMDNJ-New Jersey Medical School, Newark 07103-2714.
Mol Cell Biol (UNITED STATES) May 1992, 12 (5) p2273-81, ISSN 0270-7306 Journal Code: NGY

Contract/Grant No.: AG 04821, AG, NIA; RO1-ES(CA)-05735, ES, NIEHS
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Human diploid fibroblasts have a limited life span in vitro, and spontaneous immortalization is an extremely rare event. We have used transformation of human diploid fibroblasts by an origin-defective simian virus 40 genome to develop series of genetically matched immortal cell lines to analyze immortalization. Comparison of a preimmortal transformant (SVtsA/HF-A) with its uncloned and cloned immortalized derivatives (AR5 and HAL) has failed to reveal any major alteration involving the simian virus 40 genome. Karyotypic analysis, however, demonstrated that all of the immortal cell lines in this series have alterations of **chromosome** 6 involving loss of the portion distal to 6q21. The karyotypic analysis was corroborated by DNA analyses. Southern analysis demonstrated that only one copy of three proto-oncogene loci (ros1, c-myb, and mas1) on 6q was retained in immortal cells. Polymerase chain reaction analysis of the microsatellite polymorphism at 6q22 (D6S87) showed loss of heterozygosity. In addition, elevated expression of c-myb (6q22-23) was observed. We hypothesize that the region at and/or distal to 6q21 plays a role in immortalization, consistent with the presence of a growth suppressor gene.

2/3,AB/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07306939 92345591
Correlation of CD2 expression with PML gene breakpoints in patients with acute promyelocytic leukemia [see comments]
Claxton DF; Reading CL; Nagarajan L; Tsujimoto Y; Andersson BS; Estey E; Cork A; Huh YO; Trujillo J; Deisseroth AB
Department of Hematology, University of Texas M.D. Anderson Cancer Center, Houston 77030.
Blood (UNITED STATES) Aug 1 1992, 80 (3) p582-6, ISSN 0006-4971
Journal Code: A8G
Contract/Grant No.: PO1 CA55164-01A1, CA, NCI
Comment in Blood 1993 Mar 15;81(6):1666
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The **chromosomal translocation** t(15;17)(q22:21) of acute promyelocytic leukemia (APL) fuses PML, a novel gene, with RAR alpha, a retinoic acid receptor gene. PML-RAR hybrid transcripts were studied in 18 cases of APL using **RNA**-PCR. Two forms were noted: one designated 5', producing a 439-bp chimeric fragment, and a 3' form, producing a pair of fragments of 765 bp and 909 bp. 5' forms were found in 7 of the 18 cases while the other 11 patients expressed the 3' forms. The **chromosome** 15 specific probes K3 and K2 were used to study genomic breakpoints in 12 APL patients. Comparison of these results with **RNA** PCR in 11 patients for whom both were available yielded a rearrangement pattern predictive of whether the hybrid transcript was 5' or 3'. In this way, an additional three patients in whom DNA but not **RNA** was available were identified as having 3' (downstream) breakpoints and, therefore, 3' hybrid forms. Thus, 21 cases categorized as having 5' or 3' PML-RAR transcripts were analyzed for various phenotypic differences. Surface phenotyping of leukemic promyelocytes demonstrated expression of the CD2 antigen in all cases with the 5' splice variant. Only 1 of 11 cases with the 3' form showed CD2 expression. This difference is significant at P = .001.

2/3,AB/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07105724 92334332
Can, a putative oncogene associated with myeloid leukemogenesis, may be

Elefanty AG; [redacted]riharan IK; Cory S
Walter and [redacted]iza Hall Institute of Medic[redacted] Research, Royal Melbourne Hospital, Victoria, Australia.
EMBO J (ENGLAND) Apr 1990, 9 (4) p1069-78, ISSN 0261-4189 Journal Code: EMB
Contract/Grant No.: CA 12421, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE

The **chromosome translocation** forming the hybrid bcr-abl gene is thought to be the initiating event in chronic myeloid leukaemia (CML) and some cases of acute lymphoblastic leukaemia. To assess the impact of bcr-abl upon haemopoiesis, lethally irradiated mice were reconstituted with **bone marrow** cells enriched for cycling stem cells and infected with a bcr-abl bearing retrovirus. The mice developed several fatal diseases with abnormal accumulations of macrophage, erythroid, mast and lymphoid cells, and marked strain differences in disease distribution and kinetics. Some mice exhibited more than one neoplastic cell type and, in some instances, these were clonally related, indicating that a progenitor or stem cell had been transformed. While classical CML was not observed, the macrophage tumours were accompanied by a mild CML-like syndrome, probably due to myeloid growth factor production by tumour cells. The erythroid and mast cell diseases were rarely transplantable, in contrast to the macrophage tumours and lymphomas, but all disease types displayed limited clonality. These results establish that bcr-abl confers a proliferative advantage on diverse haemopoietic cells but complete transformation probably involves additional genetic changes.

2/3,AB/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06598644 90353953
Identification and characterization of transcripts from the neurofibromatosis 1 region: the sequence and genomic structure of EVI2 and mapping of other transcripts.
Cawthon RM; O'Connell P; Buchberg AM; Viskochil D; Weiss RB; Culver M; Stevens J; Jenkins NA; Copeland NG; White R
Howard Hughes Medical Institute, University of Utah, Salt Lake City 84132.
Genomics (UNITED STATES) Aug 1990, 7 (4) p555-65, ISSN 0888-7543 Journal Code: GEN
Contract/Grant No.: N01-CO-74101, CO, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Mapping of the EVI2 gene between the **translocation** breakpoints of two patients with neurofibromatosis type 1 (NF1), combined with the likely role of its murine homolog in neoplastic disease, implicates EVI2 as a possible candidate for the NF1 gene. We report here the expression of a 1.6-kb EVI2 transcript in normal human brain and peripheral **blood** mononuclear cells. Sequencing studies predict an EVI2 protein of 232 amino acids that contains an N-terminal signal peptide, an extracellular domain with five potential glycosylation sites, a single hydrophobic transmembrane domain with a leucine zipper, and a hydrophilic cytoplasmic domain. These features are all well-conserved with respect to the mouse Evi-2 protein and are consistent with the hypothesis that EVI2 is a membrane protein that may complex with itself and/or other proteins within the membrane, perhaps to function as part of a cell-surface receptor. In the course of these studies we have also identified three other transcripts (classes of cDNAs) from the NF1 region. Two of these transcripts map between the NF1 **translocation** breakpoints; the remaining transcript maps just outside this region.

2/3,AB/15 (Item 15 from file: 155)

DIALOG(R)File 1[redacted]MEDLINE(R)
(c) format only[redacted]99 Dialog Corporation. All rts[redacted]eserv.

06458934 90199880
The candidate proto-oncogene bcl-3 is related to genes implicated in cell lineage determination and cell cycle control.
Ohno H; Takimoto G; McKeithan TW
Department of Pathology, University of Chicago, Illinois 60637.
Cell (UNITED STATES) Mar 23 1990, 60 (6) p991-7, ISSN 0092-8674
Journal Code: CQ4
Contract/Grant No.: CA49207, CA, NCI; CA42557, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
A gene, bcl-3, is found on **chromosome** 19 adjacent to the breakpoints in the **translocation** t(14;19)(q32;q13.1), which occurs in some cases of chronic lymphocytic leukemia. Sequence analysis of the human bcl-3 gene predicts a protein containing seven tandem copies of the SWI6/cdc10 motif. This motif was previously identified in yeast genes that regulate events at the start of the cell cycle and in invertebrate transmembrane proteins involved in cell differentiation pathways. Expression of bcl-3 in normal **blood** cells increases markedly following mitogenic stimulation, and leukemic cells with the **translocation** show much greater expression than controls. These results suggest that bcl-3 is a proto-oncogene that may contribute to leukemogenesis when abnormally expressed.

2/3,AB/16 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11470260 BIOSIS NO.: 199800251592
Identification and **purification** of the Holo-ELL complex: Evidence for the presence of ELL-associated proteins that suppress the transcriptional inhibitory activity of ELL.

AUTHOR: Shilatifard Ali(a)
AUTHOR ADDRESS: (a)St. Louis Univ. Sch. Med., Edward A. Doisy Dep. Biochem. Mol. Biol., 1402 South Grand Blvd., St., USA

JOURNAL: Journal of Biological Chemistry 273 (18):p11212-11217 May 1, 1998
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The human ELL gene on **chromosome** 19 undergoes frequent **translocation** with the trithorax-like MLL gene on **chromosome** 11 in acute myeloid leukemia. Recently, it was demonstrated that the product of the human ELL gene encodes an **RNA** polymerase II elongation factor (Shilatifard, A., Lane, W. S., Jackson, K. W., Conaway, R. C., and Conaway, J. W. (1996) Science 271,1873-1876). In addition to its elongation regulatory activity, ELL contains a novel type of **RNA** polymerase II interaction domain that is capable of negatively regulating polymerase activity in promoter-specific transcription in vitro (Shilatifard, A., Haque, D., Conaway, R. C., and Conaway, J. W. (1997) J. Biol. Chem. 272, 22355-22363). Here, we report the identification and **purification** of a large ELL-containing complex that contains three proteins in addition to ELL and that we have named the Holo-ELL complex. The Holo-ELL complex can increase the catalytic rate of transcription elongation by **RNA** polymerase 11. However, unlike the ELL polypeptide alone, the Holo-ELL complex is not capable of negatively regulating polymerase activity in promoter-specific transcription in vitro. The inability of the Holo-ELL complex to negatively regulate polymerase activity in promoter-specific

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          391397  CHROMOSOM?
           91812  TRANSLOCAT?
            7620  CHROMOSOM?(N)TRANSLOCAT?
          462753  REVIEW
      S1     224  CHROMOSOM? (N) TRANSLOCAT? AND REVIEW
? s s1 and human

             224  S1
        11011733  HUMAN
      S2     198  S1 AND HUMAN
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or (9(w)11) or (9(w)22) or (11(w)14) or (11(w)19) or (11(w)22) or (12(w)21)
or (14(w)18) or (15(w)17)

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or (9(w)11) or (9(w)22) or (11(w)14) or (11(w)19) or (11(w)22) or (12(w)21)
or (14(w)18) or (15(w)17))

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(12(w)21) or (14(w)18) or (15(w)17))

Processing
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             198  S2
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          375484  19
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         2913872  5
          232616  2(W)5
         4147147  2
          632396  13
           11301  2(W)13
         2718260  4
          722861  11
           11801  4(W)11
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          523403  21
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         1094245  9
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         1094245  9
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            2985  9(W)22
          722861  11
          712710  14
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                 OR (11(W)19) OR (11(W)22) OR (12(W)21) OR (14(W)18) OR
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      S4      28  RD (unique items)
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 4/3,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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09844154   99139884
  The role of TEL fusion genes in pediatric leukemias.
  Rubnitz JE; Pui CH; Downing JR
  Department of Hematology/Oncology, St Jude Children's Research Hospital,
University of Tennessee College of Medicine, Memphis 38105-2794, USA.
  Leukemia (ENGLAND)  Jan 1999,  13 (1) p6-13,  ISSN 0887-6924
Journal Code: LEU
  Contract/Grant No.:  CA-71907, CA, NCI; CA-20180, CA, NCI; CA-36401, CA,
NCI; +
  Languages: ENGLISH
  Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL
  The TEL and AML1 genes are common targets of chromosomal
translocations in hematopoietic malignancies. The TEL-AML1 fusion
gene, created by the t(12;21), is the most common genetic
alteration in childhood acute lymphoblastic leukemia and is associated with
a favorable outcome. This review summarizes the roles of the TEL and
AML1 proteins in hematopoiesis, the potential transforming mechanisms of
TEL fusion proteins, and the clinical significance of the TEL-AML1 fusion.


 4/3,AB/2     (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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09744053   99052582
  [Detection of residual disease in follicular lymphomas using the PCR
technique: importance of clono-specific probes]
  Detection de la maladie residuelle dans les lymphomes folliculaires par
la technique de PCR: interet des sondes clono-specifiques.
  al Saati T; Galoin S; Roda D; Huynh A; Attal M; Delsol G
  Laboratoire d'anatomie pathologique et UPCM/CNRS, CHU-Purpan, Toulouse,
France.
  Bull Cancer (FRANCE)  Oct 1998,  85 (10) p847-54,  ISSN 0007-4551
Journal Code: BDZ
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Languages: FRENCH Summary Languages: ENGLISH
Document ty[redacted] JOURNAL ARTICLE; REVIEW; [redacted]IEW, TUTORIAL English Abstract

Follicular lymphoma constitutes 30-40% of non-Hodgkin's lymphomas. Most patients have widespread disease at diagnosis. The clinical course is generally indolent, and it is not usually curable with available treatment. The source of relapse in patients who achieve complete clinical remission is residual neoplastic cells that are present below the limits of detection using standard techniques. With the development of PCR technology, the presence of these residual malignant cells [Minimal Residual Disease (MRD)] has been demonstrated clearly. Recently, an association of high-dose chemotherapy with autologous bone marrow or peripheral blood progenitor cell autograft appeared promising in the treatment of these lymphomas. In the search of clonal markers for the detection of MRD in follicular lymphomas, two strategies can be used. In the cases associated with the t(**14;18**) (q32;q21) **chromosomal translocation** , the bcl-2/JH junctional regions are amplified by PCR in approximately equal to 50% of cases and then sequenced in order to synthesize an anti-junction oligonucleotide probe specific for each patient's malignant clone (clonospecific probe). In the cases negative for this translocation, an alternative strategy consists in the amplification of immunoglobulin high chain (IgH) gene rearrangement (approximately equal to 75% of cases). The present **review** highlights the value of molecular markers such as bcl-2/JH and VH/JH rearrangements to follow the neoplastic clone and to detect MRD in patients with follicular lymphomas.

4/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09627338 98385009
Molecular pathogenesis of childhood acute lymphoblastic leukemia.
Biondi A; Masera G
Clinica Pediatrica, Universita di Milano, Italy.
Haematologica (ITALY) Jul 1998, 83 (7) p651-9, ISSN 0390-6078
Journal Code: FYB
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, ACADEMIC

This concise **review** focuses on the most recent advances in understanding molecular genetic abnormalities in childhood acute leukemia (ALL). An increasing number of **chromosomal translocations** associated to distinct molecular genetic abnormalities have been described. Recurrent motifs have been recognized behind the great heterogeneity of genes involved in **chromosomal translocations** occurring in childhood ALL. The expression or activation of specific genes encoding for transcription factors have been recognized to be the most frequent recurring mechanism. In addition to the identification of genes involved in translocations, the analysis of deleted or mutated genes has provided new insights into the molecular pathogenesis of childhood ALL. The understanding of the genetic heterogeneity has turned out to have great impact on routine diagnosis and treatment. Molecular analysis has revealed that the t(**12;21**) translocation, barely detectable when searched for by conventional cytogenetic techniques, is the most frequent genetic lesion occurring in childhood ALL. Accumulating evidence clearly indicates that molecular characterisation at diagnosis represents the most relevant prognostic information for risk stratification of the patients at diagnosis. Several target genes are now available for the study of minimal residual disease and to evaluate its potential impact for tailoring treatment. Finally, our progress in understanding the relationships between genetic lesions and environmental etiologic agents will further contribute to delineating the natural history of pediatric ALL.

4/3,AB/4 (Item 4 from file: 155)

DIALOG(R)File 155:MEDLINE(R)
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09615831 97403233
Implication of cyclin D1 in malignant lymphoma.
Callanan M; Leroux D; Magaud JP; Rimokh R
Laboratoire GRL, Institut Albert Bonniot, La Tronche, France.
Crit Rev Oncog (UNITED STATES) 1996, 7 (3-4) p191-203, ISSN 0893-9675 Journal Code: A1Y
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL
The **chromosomal translocation** t(**11**;**14**)(q13;q32) is observed in a number of lymphoid malignancies but is specifically associated with a particular subtype of non-Hodgkin's lymphoma called mantle cell lymphoma, where it is observed in up to 70% of cases. This translocation juxtaposes IGH sequences at 14q32 to a region variously termed BCL1/PRAD1 at 11q13, on the derivative chromosome 11. Detailed molecular analysis identified BCL1 to be a gene coding for the G1 cyclin, cyclin D1, which is an important regulator of the G1/S transition of the cell cycle. Cyclin D1 overexpression is observed in a vast majority of mantle cell lymphoma and lymphoid malignancies with 11q13 rearrangement, thereby confirming BCL1, now referred to as CCND1, as the gene targeted by these rearrangements. In this **review**, following a brief discussion of the role of cyclin D1 in cell cycle regulation, we discuss the mechanisms and pathogenetic impact of cyclin D1 activation in lymphoproliferative disorders with 11q13 rearrangement. We also **review** a number of the diagnostic strategies available for detection of CCND1 rearrangement/overexpression, with particular emphasis on applications for mantle cell lymphoma.

4/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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09494941 98231657
Chromosomal translocations involving paired box transcription factors in **human** cancer.
Barr FG
Department of Pathology, University of Pennslvania School of Medicine, Philadelphia 19104-6082, USA.
Int J Biochem Cell Biol (ENGLAND) Dec 1997, 29 (12) p1449-61, ISSN 1357-2725 Journal Code: CDK
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL
The PAX genes encode a family of transcription factors that control development within the neural, myogenic, lymphoid, and a variety of other lineages. These proteins are postulated to regulate expression of gene products that function in the control of cellular processes are fundamental to the development of cancer, and thus genetic alterations of these genes may contribute to neoplastic development within these lineages. In support of this premise, several PAX genes have been shown to be targets of consistent **chromosomal translocations** associated with specific tumor types. The t(**2**;**13**) and t(1;13) translocations associated with the myogenic soft tissue cancer alveolar rhabdomyosarcoma fuse portions of the PAX3 or PAX7 gene with a portion of the FKHR gene to generate novel fusion proteins. The t(9;14) translocation associated with the B cell tumor lymphoplasmacytoid lymphoma juxtaposes the PAX5 gene into the vicinity of the IGH locus to deregulate PAX5 expression. This **review** will examine the molecular basis of these translocations and the role of altered function or expression of paired box transcription factors in the process of tumorigenesis.

4/3,AB/6 (Item 6 from file: 155)

DIALOG(R)File 155:MEDLINE(R)
(c) format only 1999 Dialog Corporation. All rts. reserv.

09490116 98211751
Frequency and clinical significance of cytogenetic abnormalities in pediatric T-lineage acute lymphoblastic leukemia: a report from the Children's Cancer Group.
Heerema NA; Sather HN; Sensel MG; Kraft P; Nachman JB; Steinherz PG; Lange BJ; Hutchinson RS; Reaman GH; Trigg ME; Arthur DC; Gaynon PS; Uckun FM
Department of Medical and Molecular Genetics, Indiana University School of Medicine, Indianapolis 46202-5251, USA. nheerema@medgen.iupui.edu
J Clin Oncol (UNITED STATES) Apr 1998, 16 (4) p1270-8, ISSN 0732-183X Journal Code: JCO
Contract/Grant No.: CA-13539, CA, NCI; CA-60437, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
PURPOSE: Nonrandom **chromosomal translocations** are frequently observed in pediatric patients with acute lymphoblastic leukemia (ALL). Specific translocations, such as t(**4;11**) and t(**9;22**), identify subgroups of B-lineage ALL patients who have an increased risk of treatment failure. The current study was conducted to determine the prognostic significance of **chromosomal translocations** in T-lineage ALL patients. MATERIALS AND METHODS: The study included 169 children with newly diagnosed T-lineage ALL enrolled between 1988 and 1995 on risk-adjusted protocols of the Children's Cancer Group (CCG) who had centrally reviewed cytogenetics data. Outcome analyses used standard life-table methods. RESULTS: Presenting features for the current cohort were similar to those of concurrently enrolled patients for whom cytogenetic data were not accepted on central **review**. The majority of patients (80.5%) were assigned to CCG protocols for high-risk ALL and 86.4% had pseudodiploid (n = 80) or normal diploid (n = 66) karyotypes; modal chromosome number was not a significant prognostic factor. Overall, 103 of 169 (61%) patients had an abnormal karyotype, including 31 with del(6q), 29 with 14q11 breakpoints, 15 with del(9p), 11 with trisomy 8, nine with 11q23 breakpoints, nine with 14q32 translocations, and eight with 7q32-q36 breakpoints. Thirteen patients had the specific 14q11 translocation t(**11;14**)(p13;q11) and all were classified as poor risk. Patients with any of these translocations had outcomes similar to those with normal diploid karyotypes. CONCLUSION: Chromosomal abnormalities, including specific nonrandom translocations, were frequently observed in a large group of children with T-lineage ALL, but were not significant prognostic factors for this cohort. Thus, contemporary intensive treatment programs result in favorable outcomes for the majority of T-lineage ALL patients, regardless of karyotypic abnormalities, and such features do not identify patients at higher risk for relapse.

4/3,AB/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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09305364 98003002
Immunohistochemical and molecular genetic approaches to soft tissue tumor diagnosis: a primer.
Hibshoosh H; Lattes R
Department of Pathology, College of Physicians and Surgeons Columbia University New York, NY 10032, USA.
Semin Oncol (UNITED STATES) Oct 1997, 24 (5) p515-25, ISSN 0093-7754 Journal Code: UN5
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL
During the past two decades we have witnessed the identification of an expanding list of immunohistochemical and molecular markers linked to histopathologically defined subtypes of tumors. These markers offer new